

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 164310

TO: Jon E Angell

Location: 2d20 / 2c18

Friday, September 02, 2005

Art Unit: 1635

Phone: 571-272-0756

Serial Number: 09 / 972916

From: Jan Delaval

Location: Biotech-Chem Library

Remsen 1a51

Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes			



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Fro	m:
~ 4	1

Chan, Christina

To:

Angell, Jon E; STIC-Biotech/ChemLib

Subject:

RE: RUSH Sequence Search Request 09/972,916

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 (571)-272-0841 Remsen, 3E89

-----Original Message-----

From:

Angell, Jon E

Sent:

Tuesday, August 30, 2005 11:24 AM

To:

Chan, Christina ·

Subject:

RUSH Sequence Search Request 09/972,916

I would like to request a RUSH sequence search because this case is an after final amended case that was forwarded to me 8/29/2005.

If approved, please forward the request to STIC and CC a copy to me, THANKS!

SEARCH REQUEST FORM

Scientific and Technical Information Center

Examiner#: 78697

Art Unit: 1635

Phone Number: 571-272-0756

Date: 8/30/2005

Serial Number: 09/972,916 (THULE et al.)

Mailbox & Bldg/Room Location: REMSEN 2C18

Results Format Preferred (circle): Paper

I would like to have a standard search of the nucleic acid databases including the pending applications databases (i.e., an interference search) performed using the following SEQ. ID NOs. from application: 09/972,916

SEQ ID NO: 1 (nucleic acid 51 nucleotides in length)

SEQ ID NO: 2 (nucleic acid 219 nucleotides in length)

SEQ ID NO: 3 (nucleic acid 270 nucleotides in length)

SEQ ID NO: 4 (nucleic acid 321 nucleotides in length) SEQ ID NO: 5 (nucleic acid 372 nucleotides in length) SEQ ID NO: 6 (nucleic acid 423 nucleotides in length)

Please note that the above sequence are gene expression regulatory sequences and the claims encompass nucleic acid sequences comprising any 1 or more of the above sequences.

STAFF USE-ONLY Searcher: Searcher Phone: 2- 3504 Date Searcher Picked up: 8 366 Date Completed: \$12/05 Searcher Prep/Rev. Time: (5 Online Time:_

Type of Search

Interference: _ Oligomer: Encode/Transl:

Structure#: Inventor: __ Litigation:_ Vendors and cost where applicable DIALOG: QUESTEL/ORBIT:

LEXIS/NEXIS:_ SEQUENCE SYSTEM: _ C

WWW/Internet: Other(Specify):

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9. Eric Augell Art Unit 1635 Office: REMSEN 2D20 mailbox: REM 2C18 571-272-0756

STAFF USE ONLY

Searcher: _____Searcher Phone: 2Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: ____
Online Time: _____

Type of Search

NA#:	AA#:
Interference:	SPDI:
S/L:	Oligomer:
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Structure#:_	Text:
Inventor:	Litigation:

Vendors and cost where applicable
STN:
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SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

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ALIGNMENTS

RESULT 1
ABX15372
ID ABX1 Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic. 08-AUG-2002. US2002107198-A1. Rattus norvegicus. Rat insulin-sensitive element (ISE) DNA. ABX15372; ABX15372 standard; DNA; 219 BP. 17-APR-2003 (first entry)

10-OCT-2001; 2001US-00972916

11-OCT-2000; 2000US-0239113P

(THUL/) THULE P M.

Thule PM;

WPI; 2002-674190/72.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells. ä

Claim 8; Page 13; 37pp; English.

The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth

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RESULT 2
ABX15373
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Matches 219
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Thule PM
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                                                                                         (THUL/) THULE
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The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to cincrease fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions CC indiabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, CC thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-constition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence cc represents a rat insulin regulator construct of the invention
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 13-14; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
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    270
  BP;
63 A;
  95 C;
  65 G;
47 T;
0 U;
  0 Other;
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232
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                                                                                                                                   52
                                                                                                                                                                              al Similarity
219; Conserv
            AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                        TCACAAGCAAAACAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                               CCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                   TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA 111
AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                           CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                             100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                         Score 219; DB 6;
Pred. No. 2.7e-60;
                                                                                                                                                                              Mismatches
                                                                                                                                                                              0
                     219
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270
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RESULT 3
ABX15374
ID ABX1
XX ABX1
XX ABX1
XX ABX1
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                                                                                                                                         Synthetic
                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat insulin regulator construct
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US2002107198-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor binding protein-1 (IGFBB-1) basal promoter: The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorricoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may at effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
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Best Local
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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1;
                                                                Rat insulin regulator construct DNA #3.
                                                                                                                                        17-APR-2003
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                                                                                                                                                                                                                                                                   ABX15375 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCACAAGCAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 BP; 77 A; 111 C; 84 G; 49 T; 0 U; 0 Other;
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Pred. No. 2.9e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin (CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to cincrease fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions CC in diabetics during short-term fasting, large carbohydrate loads or when CC diabetics during short-term fasting, large carbohydrate loads or when CC inhibition the long-term complications of diabetes. The properties CC differentiated hepatoma lines and insulin expression in these calls may constitute are essentially specific for hepatocytes and well-construct are essentially specific for hepatocytes and construct construct are construct toose provided by secreted insulin, e.g. cinibition of other intracellular hormone receptors. This sequence
                                                                                                                                                                                                                                                                                                      Matches 219;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in liver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 14; 37pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                             represents a rat insulin regulator construct of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                           Local Similarity
            181
                                                      274
                                                                                               121
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                                                                                                                                                                                                                                                             _
                                                                                                                                                                                                                                           TCACAAGCAAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCCCTGACAATCA
AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                                               CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                             CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                        TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
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                                                                                                                                                                                                                                                                                                                     Score 219; DB 6
Pred. No. 3e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                               the invention
            219
                                                                                                                                                                                                                                                                                                                                          Length 372;
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AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 372

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ABX15376
                                                                                                                                                                                                      CC The invention relates to an insulin regulator construct comprising a CC glucose response element (GJRE) of a liver pyruvate kinase (LPR) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used CC treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct CC carbohydrates) and glucocorticoids and inhibition by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly suglycaemic conditions CC in diabetics during short-term fasting, large carbohydrate loads or when CC in diabetics during short-term fasting, large carbohydrate loads or when CC in diabetics during the long-term complications of diabetes. The properties CC differentiated hepatoma lines and insulin expression in these cells may CC inhibition of cellular protein degradation, and inhibition, or Stimulation of other intracellular homome receptors. This sequence
                                                                                                                                 Matches 219;
                                                                                                                                                                  Query Match
                                                                                                                                                                                                  Sequence 423 BP; 81 A; 149 C; 116 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP insulin-sensitive element; ISE; basal promotter; hyperglycaemia; insulin-sensitive element; ISE; basal promotter; hypoglycaemia; glucose; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 14; 37pp; English
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                                                                                                                                                 Similarity
TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                       TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
                                                                                                                                                                                                                                      a rat insulin regulator construct of the invention
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor;
                                                                                                                             0,
                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insulin regulator construct; anabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA #4.
                                                                                                                                                                Length 423;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucocorticoid; rat;
                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGFBP-1;
insulin;
                                                                                                                             Gaps
                      120
                                                                                           60
                                                        264
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RESULT 6
ABK63701
cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-2000;
11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cell exposed to the toxin and comparing these to gene expression in unexposee
                                                                                                                                                                                                                                                                                                                                                                                                                                          global changes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                               compounds or the progression of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to methods for predicting toxic effects compounds or the progression of these toxic effects by determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                             toxin and comparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-241625/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2001;
19-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200210453-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat sequence differentially expressed in response to a hepatotoxin #1608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK63701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1608; 239pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells.
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2001US-0290645P.
2001US-0290645P.
2001US-0296336P.
2001US-0295736P.
2001US-0297457P.
2001US-0297457P.
2001US-0298884P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression; centrilobular necrosis; steatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0303459P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0222040P
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                                                                                                                                                                                                                                                                                                                                                                                                    progression of these toxic effects by determining the gene expression in tissues or cells exposed to the gene expression in unexposed tissues or cells exposed tissues or cells exposed tissues or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    줐
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    爱
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384
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RESULT 7
ADB58201
ID ADB58201
XXX ADB58201
AC ADB5
XXX TOX
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XX
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect.
                                                                                                                                                                                                                                                                                                                                                 Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002; 2002US-00060087, 15-MAR-2002; 2002US-0344045F, 15-MAR-2002; 2002US-0346055F, 30-DEC-2002; 2002US-0436643F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2003
                                                                                                                                                                                                                                                    Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JAN-2003; 2003WO-US003194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003064624-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxic; toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toxicity-related gene, SEQ ID 3227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB58201 standard; DNA; 1500 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003-689530/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOGIC
                                                                                                                                                                                                                                                ID NO 3227; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxicity assay; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.</u>
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥,
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Best Local
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                                                                                                       19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-JUL-2002;
            Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                      toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                                                                                                                                                                  10-APR-2002;
11-APR-2002;
                                                                                                                                                                                                                          10-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                                  08-APR-2002;
                                                                                                                                                                                                                                                             04-FEB-2002;
13-MAR-2002;
                                                                                                                                                                                                                                                                                               04-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Primary rat hepatocyte toxicity modelling related gene
                                                                                                                                                                                        19-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences.
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77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTTCCGCTACTAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGACTGTGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1500 BP;
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nilarity 98.7%;
Conservative (
                                                                                            2002US-0353171P.
2002US-035354P.
2002US-0370248P.
2002US-0371134P.
2002US-0371139P.
2002US-0373601P.
2002US-0373602P.
2002US-0378653P.
                                               LOGIC
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                        Porter M,
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                        Johnson
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Pred. No. 3.6e-14;
D; Mismatches 1
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                       Higgs
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                        B
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                        Castle A,
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                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:3252.
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2003-731472/69

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RESULT 9
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Best Local S
Matches 77
01-NOV-2001;
21-NOV-2001;
06-DEC-2001;
19-DEC-2001;
                                                         10-JUL-2001;
28-AUG-2001;
27-SEP-2001;
22-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                  19-JUN-2001;
10-JUL-2001;
                                                                                                                                                                22-MAY-2001;
13-JUN-2001;
                                                                                                                                                                                                                                                                       WO200295000-A2
                                                                                                                                                                                                                                                                                                                                                Toxic effect; gene expression profile; renal toxicity; toxicity marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABT41911 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express: profile of a tissue or cell sample to a database of Tox mean and non-
                                                                                                                      10-JUL-2001;
                                                                                                                                                                                                            22-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                          Toxicity modelling related rat gene SEQ ID No 1613.
                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTTCCGCTACTAGCTA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1500
                                                                                                                                                                                                                                                                                                                                drug
          2001US-0292335P.

2001US-0297523P.

2001US-0298925P.

2001US-0303808P.

2001US-0303810P.

2001US-0315047P.

2001US-0324928P.

2001US-0330462P.

2001US-0330867P.

2001US-0331805P.

2001US-0331805P.

2001US-0331805P.

2001US-0331805P.

2001US-0331805P.

2001US-0331805P.
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                                                                                                                                                                                                                                                                                                                               screening; toxicity assay; rat; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 A; 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 380 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 10
ADP72689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method of predicting at least one toxic CC effect of a compound. The method comprises a gene expression profile of a CT issue or cell sample exposed to the compound, and comparing the gene CC information profile to a database comprising at least part of the data or information given in the specification. The methods are useful for CC predicting at least one toxic effect of a compound, predicting the cCC progression of a toxic effect of a compound, predicting the renal CC concicty of a compound, or identifying toxicity markers in tissues or CC cells exposed to known renal toxin. The genes are useful as toxicity CC markers in drug screening and toxicity assays, in monitoring disease or CC physiological states, or disease progression. This polynucleotide crepresents a rat DNA sequence relating to the toxic effect database CC described in the specification. NOTE: The sequence data for this patent CC electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2002;
21-FEB-2002;
21-FEB-2002;
15-MAR-2002;
08-APR-2002;
08-APR-2002;
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17-APR-2002;
                                                                                                                       Renal toxin progression gene
                                                                                                                                                                                                            ADP72689
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  profile to a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
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                                                                                                                                                                                                                                                                                                                                                         197 CACTTCCGCTACTAGCTA 214
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D,
                                                                                                                                                                                                            standard; DNA; 1500
                                                                                                                                                                                                                                                                                 CACTTCCGCTACTATCTA 85
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2002US-0357843P.

2002US-0357844P.

2002US-0364134P.

2002US-0370144P.

2002US-0370206P.

2002US-037024P.

2002US-0372794P.

2002US-0371679P.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                         34.9%;
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                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                         marker #1278.
                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                          Score 76.4; DB 10 Pred. No. 3.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1500;
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ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;

toxicity

marker;

Rattus norvegicus

focal segmental glomerulosclerosis

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RESULT 11
AAH22429
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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Identification; toxic; hepatotoxic; differential non-steroidal antiinflammatory drug; ds.
                                                                                                                                                                         AAH22429 standard; DNA; 5001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                             Rat insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                    AAH22429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11;
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Elashoff M;
                                                                                                22-AUG-2001
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                                                                                                                                                                                                                                                                    CACTTCCGCTACTATCTA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porter MW,
                                                         growth factor binding protein nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          34.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76.4; D
Pred. No. 3.6e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
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                   gene expression; NSAID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1500;
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                                                                                                               The present invention describes a method of screening a test agent for CC hepatotoxicity. The method comprises: (a) providing a test cell copullation comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKMARKER 1-8 and INJURYMARKER 1-10; (b) contacting the test cell population with a test ce gent; (c) measuring expression of one or more of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKMARKER cor INJURYMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a diffication of the patotoxic agent. The present sequence is given in the exemplification and reference cell population.
                                       Matches
                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1999;
18-FEB-2000;
20-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression with reference population and identifying difference in expression
                                                                                                             Sequence
                                                                                                                                               of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 22-24; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP
                                       77;
                                                       Similarity
 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 196
                                                                                                           5001 BP; 1225 A; 1204 C; 1261 G;
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0183531P.
2000US-00717321.
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                                                     34.9%;
                                       0,
                                                    Score 76.4; DB 4;
Pred. No. 5.3e-14;
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramseh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.
                                                                                                             1311
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                                                                                                             T;
                                                                      Length 5001;
                                       Indels
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                                                                                                             Other;
                                       <u>.</u>
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                                       Gaps
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밁 S 197 61 CACTTCCGCTACTATCTA CACTTCCGCTACTAGCTA 214 78

В

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CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC

60

RESULT 12 ABN95896 ABN95896 standard; DNA; 6128

ВP

13-AUG-2002 (first entry)

Gene #2394 used to diagnose liver cancer.

metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism. Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;

Homo sapiens

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RESULT 13
ABV75371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABM93503-ABM97455 in a tissue sample. The method of the invention has hepatotropic, and cyvostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                               Insulin-like growth factor binding protein; IGFBP; cytostatic; liver;
cancer; human; IGFBP-1; gene; ds.
                                                                                Human IGFBP-1
                                                                                                                07-MAR-2003
                                                                                                                                               ABV75371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6128 BP; 1504 A; 1497 C; 1504 G; 1623 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing and detecting the progression carcinoma or metastatic liver tumor in a
   Homo sapiens
                                                                                                                                                                           ABV75371 standard; DNA; 6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2394; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-426119/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                          645
                                                                                                                                                                                                                                                                                                                       593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of expression of two or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT
                                                                                                                                                                                                                                                                                      CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202
                                                                                                                                                                                                                                                                                                                       GAGCATCGGCCACCGCCATCC
                                                                                                                                                                                                                                                                                                                                                   CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                                                                                                                                                                                                                                                                                    TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTAGCAAAACAAACTTATTTTGAACACTCAGCTCCTAGCGTGCGGCGCGCCCAATCAT
                                                                                                                                                                                                                                                          CCACCCTCCCAGAGAGCACTGGCCACCGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                               gene
                                                                                                            (first entry)
                            IGFBP-1; gene; ds
                                                                               sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 ------GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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No. 5
                                                                                                                                                                                                                                                                                                                       CATCCAGCGAGCATCTGCCGCCGCGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of liver cancer, hepatocellular patient, involves detecting the in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .9e-09;
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                                                                                                                                                                                                                                                          676
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                                                                                  Best Local
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                                                                                                                                          The invention relates to detecting the presence or diagnosing the risk of a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGPBP). The method is useful for detecting the presence or diagnosing the risk of a liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGPBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
                                                                                                                                                                                                                                                                                                  Detecting the presence or diagnosing the risk of a liver cancer in patient comprises detecting aberrant expression of a gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cbs
                                                                                                                     Sequence 6128
                                                                                                                                                                                                                                                                 Example; Page 104-108; 142pp; English.
                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                          Huynh TH, Chow PKH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                03-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                              (NACA-) NAT CANCER CENT SINGAPORE PTE LTD. (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200290580-A1
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                                                                                                                                                                                                                                                                                       insulin-like growth factor binding protein.
                        473
 62
                                                N
                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 SINGAPORE GEN HOSPITAL PTE ARGAET V P.
  TAACCC---
                                                CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT 61
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0288441P
                                                                                                                     BP; 1504 A; 1497 C;
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/number= 2
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/*tag= c
/number= 1
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4170. .5068
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/*tag= f
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/*tag= d
/number= 2
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/product= "IGFBP-1"
/note= "insulin-like growth factor binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'number= 4
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/number= 3
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                                                                                  27.8%;
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-GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC 111
                                                                                                                                                                                                                                                                                                                                                                           ក្ត
                                                                       <u>.</u>
                                                                                  Score 60.8; DB 10 Pred. No. 5.9e-09;
                                                                        Mismatches
                                                                                                                     1504 G;
                                                                                             DB 10;
                                                                                                                     1623 T; 0 U; 0 Other;
                                                                        Indels
                                                                                             Length 6128;
                                                                     19;
                                                                     Gaps
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                        532
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2 CACAAGCAAAACATATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT 61	ş
Query Match 27.8%; Score 60.8; DB 4; Length 6134; Best Local Similarity 66.5%; Pred. No. 5.9e-09; Matches 141; Conservative 0; Mismatches 52; Indels 19; Gaps 3;	3 00 0
Sequence 6134 BP; 1505 A; 1498 C; 1507 G; 1624 T; 0 U; 0 Other;	ő
C gene profile can be used for diagnosis, prognosis or monitoring of C treatments and for investigating a predisposition to a disorder where the C gene is associated with a cancer, immunopathology or neuropathology	2222
to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The	i i i i
embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used	ដែកដ
fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of	ដែកដ
assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their	កក
proteins (II) encoded by then are used in high throughput screening	កកក
AAH57161 to AAH57576 represent cell and tissue specific polynucleotide	វឥន
Claim 1; Page 246-248; 327pp; English.	Š
New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology.	2444
WPI; 2001-291057/30.	X X !
Sornasse T, Seilhamer JJ, Watson GA;	Ωŭ:
(INCY-) INCYTE GENOMICS INC.	× × 5
04-NOV-1999; 99US-0163508P.	3 % 5
02-NOV-2000; 2000WO-US030396.	3 4 5
10-MAY-2001.	₹ 8
WO200132927-A2.	Z Z
Homo sapiens.	₹ % ;
Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory; neuroprotective; gene therapy; cancer; immunopathology; neuropathology.	85555
Human liver cell specific cDNA sequence SEQ ID NO:329.	요표
10-SEP-2001 (first entry)	233
AAH57489;	₹ก:
RESULT 14 AAH57489 ID AAH57489 standard; cDNA; 6134 BP.	26 ₹ 8
645 CCACCCTCCCAGAGAGCCACTGGCCACCGCTCC 676	용
171 CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202	Ş
593 GAGCATCGGCCACCGCCATCCCATCCAGCGAGCATCTGCCGCCGCCGCCGCCG 644	မွ
CAGCATGGTCCACTGCCCGCCGAGACACACAACCCCAGCGAGCATTGAACACTGC-ACACGG 1	ş
533 TAACCTCCTGGTGCAAGTGGCGCGGGCCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGC 592	8

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RESULT 15
ABL32997/c
ID ABL32
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Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, eppllepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/unlearative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2997/c
ABL32997
                                                                                                                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisporiatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; aeurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                             Sequence
                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 970; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                    WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                  Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP007537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                           7061 BP; 1852 A; 147 C; 1865 G; 3197 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202
                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 7061
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17.3%;
llarity 73.8%;
Conservative
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2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                    Berlin
Score 37.8; DB 6;
Pred. No. 0.16;
0; Mismatches 17;
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                                                              0 U, 0 Other;
                               Length 7061;
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2 CACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT 61

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17;

Indels

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Gaps

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
         seq length: 0
seq length: 2000000000
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1: /cgn2 6/ptodata/1.

2: /cgn2 6/ptodata/1.

3: /cgn2 6/ptodata/1.

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      US-09-972-916B-1
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-949-016-117205
US-09-949-016-6094
US-08-945-140-2
US-08-975-428-1
US-08-975-428-1
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US-09-949-016-135576
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11786, A
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US-09-697-022-1 US-08-080-255-6	US-09-949-016-3977	US-09-949-016-148899	US-09-949-016-11774	US-09-902-340-1012	US-09-252-991A-11837	US-09-902-540-2799	US-09-252-991A-11608	US-09-252-991A-11759	US-09-949-016-116783	US-09-949-016-13747	US-09-949-016-15764	US-09-949-016-11932	US-09-016-434-1388	US-09-826-509-452
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1, Appli 6, Appli	3977, Ap	148899,	11774, A	14957 A	7	2799, Ap	11608, A	11759, A	116783,	13747, A	15764, A	11932, A	1388, Ap	452, App

ALIGNMENTS

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US-08-945-140-1
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/945,140
FILING DATE: US/08/945,140
FILING DATE: F14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F8 95/04558
FILING DATE: 14-APR-1995
PRIOR APPLICATION UMBER: WO PCT/FR96/00560
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Saviraby Reg. Martin F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08945140 Patent No. 6309878 GENERAL INFORMATION:
                                                                                                                           TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                          NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: E9550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEPAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 194 base pairs
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APPLICANT: DOIRON, Br
APPLICANT: KAHN, Axel
                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Rhone-Poulenc STREET: 500 Arcola Road,
                                                   nucleic acid
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Mailstop 3C43
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Query Match

100.0%;

Score 51;

DB 3;

Length 194;

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US-08-791-849A-14
                                                                  US-08-791-849A-14
Query Match
Best Local Similarity
Matches 51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08791849A Patent No. 5914449 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 13011 base pai
                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warren M. Cheek, Jr.
REGISTRATION INDMER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: January CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,849A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Makoto MURASE et al.
TITLE OF INVENTION: Method for Increasing Storage
TITLE OF INVENTION: Lipid Content in Plant Seed
                                                                                                                               FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                             FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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DEDNESS: double
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805 Fifteenth Street, N.W., #700
100.0%; ilarity 100.0%; Conservative 0
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                                                                               join(3219..3765, 3949..5916, 6009..6151, 6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910, 8078..929 9480..10162)
                                                                                                                                                                                                                                                                                                            rat (Rattus norvegicus)
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6152..6283, 6418..6604, 6921..7191, 7302..7452,
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Score 51; DB 2;
Pred. No. 9.8e-09;
Mismatches 0;
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; Mismatches 0;
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US-09-949-016-11786
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LENGTH: 15108
                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6812339
                                                                                                                                                                                                                                             PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                TYPE:
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les 39; Conserv
                2357 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 2399
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                                                                                                                                                                            DNA
                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.8%; ilarity 90.7%; Conservative
                                                                               Conservative
                                                                                                                                                                                                                                                            2000-09-08
                                                                                              71.8%;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17205
LENGTH: 15108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11786, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCCAGTGTA 51
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                                                                                                   Score 36.6; DB 4; Length 15108; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36.6; DB 4
Pred. No. 0.0012;
0; Mismatches
                                                                           Mismatches
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; NAME/KEY: gene
; LICATION: (0):..(0)
; OTHER INFORMATION: Zic 1 Protein gene; Genbank Acession D76435
US-09-234-332-5
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APPLICANT: Ceddars-Sinai Medical Center

APPLICANT: Michel F. Levesque, M.D.

APPLICANT: Michel F. Levesque, M.D.

APPLICANT: TOOMAS Meuman, Ph.D.

TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO

TITLE OF INVENTION: NEURONS; TRANSDIFFERNTIATION OF EPIDERMAL CELLS

FILE REFERENCE: P07 41494

CURRENT APPLICATION NUMBER: US/09/234,332A

CURRENT FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 3138

TYPE: NA
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Best Local Similarity
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                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION UMBER: FR 95/04558
PILING DATE: 14-APR-1995
PRIOR APPLICATION NUMBER: WO PCT/FR96/00560
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SAVILEKY ESQ., MARCIN F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: EX9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DOIRON, Br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHEN, Ruihuan
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19426
                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Collegeville
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73.8%;
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    EX95002-US
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Pred. No. 20;
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TOPOLOGY: 11;
MOLECULE TYPE:
US-08-775-428-1
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Query Match 47.1%;
Best Local Similarity 75.0%;
Matches 30; Conservative
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Best Local Similarity
Matches 24; Conserv
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TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sathe, Ganesh
APPLICANT: Fuetterer, Wendy
APPLICANT: Bergsma, Derk
APPLICANT: Ellis, Catherine
TITLE OF INVENTION: CDNA CLONE HNFJD15 THAT ENCODES
                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1498 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: AT TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FABLSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 09-JAN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CDNA CLONE HNFJD15 THAT ENCULES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 19406
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               TELEFAX: 610-270-4060
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: King of Prussia
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Score 24; DB 2; Length 1498; Pred. No. 25; O; Mismatches 10; Indels
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US-09-016-434-1017/c
; Sequence 1017, Application US/09016434
; Patent No. 6500938
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 33
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SEQ ID NO 60944
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60944, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                        FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
NAME: Zeller, Karen J. REGISTRATION NUMBER: 37, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              STATE: C
                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: HEREWI
                                                                                                                                                                                                                                                                                                                                                                                                    CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                         HEREWITH
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                     37,071
    PA-0002 US
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; LENGTH: 2777;
; TYPE: DIA
; ORGANISM: Infectious pancreatic necrosis virus
US-09-282-147-39
                                                                                                                                                                                                                                                                                       RESULT 11
US-09-949-016-1956/c
                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VAKHARIA, Vikram

APPLICANT: YAO, Kun

APPLICANT: YAO, Kun

TITLE OF INVENTION: METHOD FOR GENERATING NON

TITLE OF INVENTION: FANCREATIC NECROSIS VIRUS

TITLE OF INVENTION: TRANSCRIPTS

FILE REFERENCE: 8288-9023

CURRENT APPLICATION NUMBER: US/09/282,147

CURRENT FILING DATE: 1999-03-31

EARLIER APPLICATION NUMBER: US/09/280,278

EARLIER FILING DATE: 1998-03-31

EARLIER APPLICATION NUMBER: PCT/US97/12955

EARLIER APPLICATION SUMBER: PCT/US97/12955

EARLIER APPLICATION DATE: 1998-03-31
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                                                                                                                             Sequence 1956, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Patent No. 6274147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 845-410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 659 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: CL. 930839
                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 45.9%;
Local Similarity 73.2%;
nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS PANCREATIC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%;
73.2%;
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Pred. No. 44;
0; Mismatches 11;
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Pred. No. 38;
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APPLICATION NUMBER: 60/231,498

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US-09-023-655-1294
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; ORGANISM: Human
US-09-949-016-1956
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEPHONE: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1294:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1956
LENGTH: 3078
                                                      Matches
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1294, Application US/09023655 Patent No. 6607879
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 31.
STREET: 31.
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                       IMMEDIATE SOURCE
LIBRARY: GENBA
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                           501 CGAGGCACTGACGAGAAGCCTGGAGTCTGTGCCCCAGTGCA 461
11 CGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
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                                                      Conservative
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73.2%;
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                                                                    Score 23.4;
Pred. No. 44;
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Pred. No. 44
                                                    Mismatches
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                                                                                  DB 4; Length 3088;
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILLNG DATE: 2000-09-08
NUMBER: OF SEG ID NOS: 207012
SOFTWARE: PASESEQ for Windows Version 4.0
SEG ID NO 49730
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                                                                                                                                                                            ; ORGANISM: Human
US-09-949-016-49730
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49730, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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Patent No. 6812339
                                                                                       Matches
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                                                                                                                                                                                                                                             LENGTH: 601
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                                                                                                            Local Similarity
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453
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                                                                                       31;
                         4 GGGCGCACGGGGCCCCCAG 47
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                                                                                    Conservative
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                                                                                  Score 23.2; DI
Pred. No. 44;
0; Mismatches
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Pred. No. 59;
0; Mismatches
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OF DETECTION AND USES THEREOF
                                                                                                                            Length 601;
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RESULT 15 US-09-949-016-49731/c

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Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERBOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERBOF
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION WUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2001-0-3
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-03
PRIOR PR
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run
                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
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5:
5:
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7:
9:
10:
111:
12:
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Gapop 10.0 , Gapext 1.0
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270
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19 20	15 C 16	13 11 11	7 9 10	กเมนเบล	Result No.
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ABX15375 AAT96631 ABT42448	ABX15371 ABX15374 ABX15374	AAH22429 ABN95896 ABV75371	ADB58201 ADB52710 ABT41911	ABX15376 ABX15376 ABX15374 ABX15375 ABX15372 ABX153701	ID
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The invention relates to an insulin regulator construct comprising glucose response element (GIRE) of a liver pyruvate kinase (LPK) ge

Claim 9; Page 13-14; 37pp; English.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.

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WPI; 2002-674190/72.

ALIGNMENTS

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RESULT 1
ABX15373
ID ABX1
Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoctar; hyperglycaemia; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; dlabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; callular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                               11-OCT-2000; 2000US-0239113P.
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                                                                                                                                                                                                                               08-AUG-2002.
                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                      Rattus norvegicus.
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RESULT 2
ABX15376
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Best Local Similarity
Matches 270; Conserv
11-OCT-2000; 2000US-0239113P
                                                                         08-AUG-2002
                                                                                                                                                               Rattus norvegicus.
                                                                                                                                                                                                                     glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                        Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-insulin-sensitive element; ISE; basal prometer; hyperglycaemia; insuliinsulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                10-OCT-2001; 2001US-00972916.
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                                                                                                                                                                                                      intracellular hormone
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The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties CC differentiated hepacoma lines and insulin expression in these cells may care effects additional to those provided by secreted insulin, e.g. carbohydrate intracellular hormone receptors. This sequence
                                      Best Local Sin
Matches 270;
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Best Local &
                                                                                                                      Sequence 423 BP; 81 A; 149 C; 116 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9;
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RESULT 3
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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose;

Rat insulin regulator construct

DNA #2

17-APR-2003

(first entry)

ABX15374 standard; DNA;

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                                                                                                                                     221
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281
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99.5%;
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Pred. No. 8.7e-61;
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RESULT 4 ABX15375

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                                                                                                                                The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPR) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-l (IGFBP-l) basal promoter. The construct is used CC to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperlycaemia (without severe hypoglycaemia), to cincrease fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions CC in diabetics during short-term fasting, large carbohydrate loads or when CC thus inhibiting the long-term complications of diabetes. The properties CC of the construct are essentially specific for hepatocytes and well-CC differentiated hepatoma lines and insulin expression in these cells may carbohydrate additional to those provided by secreted insulin, e.g.
                                                 Query Match
Best Local Similarity
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                                                                                                                                                                 inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
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                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (THUL/) THULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX15375 standard; DNA; 372 BP.
              50
                                                                                                                                372
TATCACAAGCAAAACAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCCCTGACAAT 109
                                               81.3%;
nilarity 99.5%;
Conservative
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                                                                                                                                BP;
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                                                                                                                              87 A; 128 C; 102 G;
                                                   <u>.</u>
                                               Score 219.4; DB 6
Pred. No. 9.2e-61;
0; Mismatches 1
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                                                                                                                              55 T; 0 U; 0 Other;
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RESULT 5
ABX15372
ID ABX11
AX ABX1
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                                                                                 in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin-sensitive element of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insuliinsulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; introduced in the control of the control
         Sequence 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 13; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-2000; 2000US-0239113P
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intracellular hormone
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         B₽;
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    A; 77 C;
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    <u>ଜ୍</u>
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37 T; 0 U; 0 Other;
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insulin;
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Query Match Best Local Similarity

100.0%; 81.1%;

Score 219; Pred. No.

DB 6; le-60;

Length 219;

The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comparising detecting the level of expression in a tissue or cell sample exposed to the compound of two comore genes listed in the specification, where differential expression. The genes is indicative of at least one toxic effect or progression. The

effect

the

progression. The

or

Claim

1:

SEQ ID NO 1608; 239pp; English.

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RESULT 6
ABK63701
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                                                                                                                                                                                                                                                                                                                           Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2000;
02-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-241625/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mendrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-2002
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2000US-0244880P.

2001US-0290029P.

2001US-0290645P.

2001US-0292336P.

2001US-0292336P.

2001US-0297457P.

2001US-0297457P.

2001US-029884P.

2001US-0303459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001WO-US023872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; EST; drug screening on; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elashoff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171
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Query Match
Best Local S
Matches 77
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15-MAR-2002; 2002US-0364055P
15-MAR-2002; 2002US-0364055P
30-DEC-2002; 2002US-0436643F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and statosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxicity-related gene, SEQ ID 3227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB58201 standard; DNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                        markers in liver tissues c
                                                                                                                                                                                                                                                                                                                                            31-JAN-2003; 2003WO-US003194
                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003064624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toxic; toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                                           Mendrick D,
                                                                                                                                                                                                     (GENE-) GENE LOGIC INC.
                                                                                                                     2003-689530/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ecreening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTTCCGCTACTATCTA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                             Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxicity assay; ds.
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98.7%;
                                                                                                                                                             Johnson
                                   t of a compound, useful in identifying toxicity or cells for drug screening and toxicity assays, expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No. 3.
                                                                                                                                                           ζ,
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                                                                                                                                                         Higgs
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                                                                                                                                                           В,
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                                                                                                                                                             Castle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1500;
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comprises preparing the compound.

gene

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RESULT 8
ADB52710
ID S2710
ID S2710
ID S2710
AC ADB5
XX ADB5
XX ADB5
XX UCXI
KW COXI
KW COXI
KW COXI
KW COXI
KW COXI
KW COXI
IXW DFIM
XX W COXI
IXW COXI
IXW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC of a tissue or cell sample exposed to the compound, and comparing the CC of a tissue or cell sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 1-4925, where CC differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect. CC compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at CC compound modulates in a cell, and identifying an agent one activity of a protein. The method and compositions of the CC present invention using a database of genes having liver toxin-induced CC differential expression, are useful in identifying toxicity markers in CC liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                            13-MAR-2002;
13-MAR-2002;
18-APR-2002;
10-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
19-APR-2002;
22-APR-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primary rat hepatocyte toxicity modelling related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB52710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3227; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTTCCGCTACTATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 67
2002US-0363534P.
2002US-0370134P.
2002US-0371135P.
2002US-0371150P.
2002US-0371413P.
2002US-0373601P.
2002US-0373602P.
2002US-0373602P.
2002US-0378370P.
2002US-0378652P.
2002US-0378653P.
2002US-0394230P.
2002US-0394253P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to a method for predicting a toxic effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0353171P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003WO-US003482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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Pred. No. 3.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1500,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:3252.
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RESULT 9
ABT41911
ID ABT4
XX ABT4
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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers ference represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                          22-MAY-2001; 2001US-0292335P.
13-JUN-2001; 2001US-0297523P.
19-JUN-2001; 2001US-0298925P.
10-JUL-2001; 2001US-0303807P.
  10-JUL-2001;
                                                                                                                                                                        22-MAY-2002;
                                                                                                                                                                                                                             28-NOV-2002
                                                                                                                                                                                                                                                                                  WO200295000-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          Toxic effect; gene expression profile; renal toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABT41911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABT41911 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1500 BP; 336 A; 408 C; 380 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2002; 2002US-0407688P.
28-JAN-2003; 2003US-0442900P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxicity modelling related rat gene SEQ ID No 1613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 44; SEQ ID NO 3252; 874pp; English
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Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-731472/69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248
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                                                                                                                                                                                                                                                                                                                                       norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                               grug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                        2002WO-US016173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOGIC INC
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                                                                                                                                                                                                                                                                                                                                                                                            screening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 1500 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.3%;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Castle A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1500;
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                                                                                                                                                                                                                                                                                                                                                                                                                             toxicity
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RESULT 10
ADP72689
ID ADP72
XX
AC ADP72
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AC ADP72
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XX
XX
AC ADP72
XX
XX
XX
AC ADP72
XX
XX

ADP72689

standard; DNA; 1500

ВP

Renal toxin

progression gene

marker #1278

26-AUG-2004 (first entry)

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                                                                                                                                                                                 The invention relates to a novel method of predicting at least one toxic CC effect of a compound. The method comprises a gene expression profile of a CC tissue or cell sample exposed to the compound, and comparing the gene CC expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for CC predicting at least one toxic effect of a compound, predicting the renal CC confictive of a compound, or identifying toxicity markers in tissues or CC cells exposed to known renal toxin. The genes are useful as toxicity CC markers in drug screening and toxicity assays, in monitoring disease or CC physiological states, or disease progression. This polynucleotide crepresents a rat DNA sequence relating to the toxic effect database CC described in the specification. NOTE: The sequence data for this patent CC calls exposed to free printed specification, but was obtained in CC electronic format directly from the World Intellectual Property
                                                                                                                      Matches
                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-UIL-2001
28-AUG-2001
27-SEP-2001
27-SEP-2001
22-OCT-2001
01-NOV-2001
21-NOV-2001
19-DEC-2001
21-PEB-2002
21-PEB-2002
21-PEB-2002
21-PEB-2002
21-PEB-2002
31-PEB-2002
08-APR-2002
08-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting at least one toxic effect modeling, comprises preparing a gene cell sample exposed to the compound,
                                                                                                                                                                                Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                           Organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     profile to a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-148464/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mendrick D,
                                                                           188 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 247
                            248 CACTTCCGCTACTAGCTA
68
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                                                                                                                                    Similarity
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CACTTCCGCTACTATCTA
                                                          CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                      Conservative
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2001US-0336144P
2001US-0340873P
2002US-0357842P
2002US-0357843P
2002US-0357844P
2002US-03541344P
2002US-0370144P
2002US-0370144P
2002US-0370206P
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2001US-0315047P.
2001US-0324928P.
2001US-0330462P.
2001US-0330867P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOGIC
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2002US-0372794P.
2002US-0371679P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC.
                                                                                                                                 28.3%;
98.7%;
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85
                            265
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                                                                                                                                    Score 76.4; DB 10 Pred. No. 3.4e-14;
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                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Higgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a compound, useful for toxicity expression profile of a tissue or and comparing the gene expression
                                                                                                                                                DB 10;
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                                                                                                                      Indels
                                                                                                                                                Length 1500;
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                                                                                                                      Gaps
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agent will induce various specific kidney pathologies, such as nephritis, kidney necrosis, glomerular and tubular injury, or focal segmental glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent. The kit is useful for predicting or modelling the toxic response of a test compound, for monitoring the progression of renal disease states, for identifying genes that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the method of the invention. (Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             effect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The methods are useful for predicting the likelihood that a compound or test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of predicting (the progression of) a toxic effect of a compound by preparing a gene expression profile of a kidney tissue or cell sample exposed to the compound and comparing the gene expression profile to a database, or detecting the level of gene(s expression in a tissue or cell sample exposed to the compound, where differential gene expression compared to a control indicates a toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 1278; 266pp; English
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                                                                        248
89
                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                    CACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                  CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                          28.3%;
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85
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                             Pred. No. 3.4e-14;
                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                            Length 1500;
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                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                              247
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RESULT 11 AAH22429 ID AAH22 XX

AAH22429 standard;

DNA; 5001

ВP

13-AUG-2002

(first entry)

ABN95896;

standard; DNA; 6128

ВP

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RESULT 12
ABN95896
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                                                                                                                                                                                                                                                                   The present invention describes a method of screening a test agent for chepatotoxicity. The method comprises: (a) providing a test cell population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKWARKER 1-8 and INJURYWARKER 1-10; (b) contacting the test cell population with a test agent; (c) measuring expression of one or more of the nucleic acid sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKWARKER cor INJURYMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification
                                                                                                                                                                                                 Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-1999;
18-FEB-2000;
20-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression
                                                                                                                                                                                                                                                                  Sequence 5001 BP; 1225 A; 1204 C; 1261 G; 1311 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 22-24; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gould-Rothberg BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-steroidal antiinflammatory drug; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification; toxic; hepatotoxic; differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin-like growth factor binding protein nucleotide sequence
                                                                                                                                                    188 CACAAACCCAGCGAGCATTGAACACTGCACACCGGCCATCTGCCCCAGAGAGCCTGTGACCAC
                                                                                                 248 CACTTCCGCTACTAGCTA
                                                                61
                                                                                                                                                                                                   77;
                                                                                                                                  \vdash
                                                                                                                                                                                                                                                                                                   present
                                                                                                                                                                                                                   Similarity
                                                                                                                                 CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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2000US-0183531P.
2000US-00717321.
                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dipippo VA,
                                                                                                                                                                                                                 28.3%;
98.7%;
                                                                    78
                                                                                                 265
                                                                                                                                                                                                   0
                                                                                                                                                                                                                   Score 76.4; DB 4;
Pred. No. 5.3e-14;
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramseh TM,
                                                                                                                                                                                                                                  DB 4;
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                                                                                                                                                                                                                                 Length 5001;
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Gene

#2394 used

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diagnose liver cancer.

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ABV75371
ID ABV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
              ABV75371
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6128 BP; 1504 A; 1497 C; 1504 G; 1623 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing and detecting the progression carcinoma or metastatic liver tumor in a level of expression of two or more genes
                                          ABV75371 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2000; 2000US-0237054P
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                   CAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                                                                                                                                                                               TAACCC-----
                                                                                                                                                                                                                                                                                                               CACTAGCAAAACAAACTTATTTTGAACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCAT
                                                                                                                                                                                                                                                                                                                                 CACAAGCAAAACAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCCCTGACAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2394; 298pp; English.
                                                                                                                                                       CCATCTGCCCAGAGAGCTGTGACCACCACTTC
                                                                                                                                                                                      GAGCATCGGCCACCGCCATCC
                                                                                                                                                                                                                                                TAACCTCCTGGTGCAAGTGGCGCCGGCCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                           DNA;
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                                           6128
                                                                                                                                                                                                                                                                               GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC
                                                                                                                                                                                                                                                                                                                                                                            0,
                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                          Score 60.8;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                      CATCCAGCGAGCATCTGCCGCCGCGCCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of liver cancer, hepatocellular patient, involves detecting the in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                            .5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 6128;
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a liver cancer in a patient. The method involves detecting in a gene biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGEBP). The method is useful for detecting the presence or diagnosing the risk of a liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver
                                                                                                                                                                                                                                                                       (NACA-)
(SIGE-)
Sequence 6128 BP; 1504 A; 1497 C;
                    encoding
                                                                                                 The invention relates to detecting the presence or diagnosing a liver cancer in a patient. The method involves detecting in
                                                                                                                                 Example; Page 104-108; 142pp; English.
                                                                                                                                                                   Detecting the presence or diagnosing the risk of a liver cancer in patient comprises detecting aberrant expression of a gene encoding
                                                                                                                                                                                                                                      Huynh TH,
                                                                                                                                                                                                                                                                                                      03-MAY-2001; 2001US-0288441P
                                                                                                                                                                                                                                                                                                                            03-MAY-2002; 2002WO-AU000558
                                                                                                                                                                                                                                                                                                                                                    14-NOV-2002
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                                                                                                                                                         insulin-like
                                                                                                                                                                                                    P-PSDB; ABB82757.
                                                                                                                                                                                                                                                           (SIGE-) SINGAPORE GEN HOSPITAL (ARGA/) ARGAET V P.
                                                                                                                                                                                                                                                                                                                                                                          WO200290580-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin-like
                                                                                                                                                                                                                2003-103522/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                    The present sequence represents a human IGF genomic DNA (GenBank Accession No. M74587)
                                                                                                                                                                                                                                                                                 NAT CANCER CENT SINGAPORE PTE LTD.
                                                                                                                                                                                                                                      Chow PKH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth factor binding protein; IGFBP; cytostatic; liver;
n; IGFBP-1; gene; ds.
                                                                                                                                                        growth factor binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene sequence.
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/number= 2
2827. .4040
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                           4170. .5068
/*tag= g
/number= 3
                                                                                                                                                                                                                                                                                                                                                                                                        5069. .5197
/*tag= h
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/*tag= c
/number= 1
2657. .2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contains
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/*tag= f
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/number= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
762. .5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product= "IGFBP-1"
note= "insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                               number= 3
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1504 G;
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1623 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                             the risk of
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Query Match

22.5%;

Score 60.8;

DB

10;

Length 6128;

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RESULT 14
AAH57489
ID AAH577
XX AAH57
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                AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical seents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH57489 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diman; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; netabolic disease; developmental disease; cytostatic; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tissue specific; diagnosis; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-291057/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 246-248; 327pp;
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           to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a
                                                                                        The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-lke growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                      New insulin regulator cassette, useful e.g. for treating provides specific, glucose-inducible transgenic expressioniver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP: insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular normone receptor; insulin regulator construct; anabolic.
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insulin;
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can maintain

euglycaemic conditions

Search completed: September 1, 2005, 00:34:43 Job time: 288.304 secs Query Match 18.9%; Score 51; DB 6; Length 51; Best Local Similarity 100.0%; Pred. No. 1.7e-06; Matches 51; Conservative 0; Mismatches 0; Indels in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat glucose response element of the invention Sequence 51 BP; 6 A; 18 C; 17 G; 10 T; 0 U; 0 Other; 0; Gaps 0,

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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene

Claim 9; Page 14; 37pp; English.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in liver cells.

WPI; 2002-674190/72.

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	Adi16493 Human NOV	Abx71176 Novel hum	Ab157731 Human sbg	Adc87210 Human GPC	Aad33646 Human TRI	Aaf94440 Human hyd	Ab157730 Human sbg	Adq51481 Novel can		Acn44410 Human gen	Abd33385 Human can		Abx04971 S. cinnam	Abz52705 Aspergill	Abn87725 Human pro		Ab190266 Human pol	Abs70481 Human bon	Ada52441 Human cod	Aas61189 Human gen	_	Huma	Rat	Abx15373 Rat insul	

ALIGNMENTS

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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                        11-OCT-2000; 2000US-0239113P.
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                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                          US2002107198-A1
                                                                                                                                                                                                                                                                                                 intracellular hormone receptor; insulin regulator construct; anabolic
                                                                                                                                                 (THUL/) THULE P M.
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                                                                                                                                                            Synthetic.
    08-AUG-2002
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                                                                                                                                                                                                                                                                                                                 cellular protein
                                                                                                                                                                                                                                                                         receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321
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                                                                                                                                                                                                                                                                                                         degradation;
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insulin;
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352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 BP; 87 A; 128 C; 102 G;
                          CTTCCGCTACTAGCTAGCCGC 321
                                                                                           CAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCACCA
                                                                                                                     TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCCGTGCTGCCGAG 180
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CTTCCGCTACTAGCTAGCCGC 372
                                                                                                                                                                                 CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGGCCGAGACA
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ilarity 100.0%;
Conservative (
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М.
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Pred. No. 4
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17-APR-2003

(first entry)

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to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hyperglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of ther intracellular hormone receptors. This sequence
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Best Local S
Matches 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 270 BP; 63 A; 95 C; 65 G; 47 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 13-14; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents a rat insulin regulator construct of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intracellular hormone receptor; insulin regulator construct; anabolic
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                                                                                                                                 GTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGC
                                                                                                                                                                                                                                                                      TGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT 160
                                                                                    TATCACAAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAAT 109
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       68.3%;
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Pred. No. 1.1e
0; Mismatches
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No. 1.1e-57
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Best Local Sin Matches 220; Query Match

Similarity

68.3%;

Score 219.4; Pred. No. Mismatches

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 Sequence
                                                                                                                                                                                                                                                                                                                        The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in
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 B₽;
                                     rat insulin regulator construct of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
 81
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A; 149 C; 116 G; 77 T;
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0 U;
   0
                                         the invention
   Other;
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CC The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC in diabetics during short-term fasting, large carbohydrate loads or when CC thus inhibiting the long-term complications of diabetes. The properties CC of the construct are essentially specific for hepatocytes and well-cCC differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1 insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein; hyperglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocritorid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                             New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                             Page 13; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insulin;
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RESULT 6
ABX15376/c
ID ABX15376 8
XX ABX15376;
XX ABX1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                         New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insuliver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin-sensitive element of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      insulin regulator construct
                                                                                                                                                                                                                                                                                                             2002-674190/72.
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                                                                                                                                                      Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                 37pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423
                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 1.4e-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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The invention relates to an insulin regulator construct comprising glucose response element (GIRE) of a liver pyruvate kinase (LPK) ge promoter and an insulin-sensitive element (ISE) of an insulin-like factor binding protein-1 (IGFBP-1) basal promoter. The construct is to treat or prevent diabetic complications, to regulate insulin

growth s used

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RESULT 7
ABK63701
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Best Local Sim:
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MOV-2000; 2000US-0244880P.
11-MAY-2001; 2001US-029029P.
15-MAY-2001; 2001US-02903645P.
22-MAY-2001; 2001US-0292336P.
06-JUN-2001; 2001US-0297457P.
13-JUN-2001; 2001US-0297457P.
19-JUN-2001; 2001US-039884P.
09-JUL-2001; 2001US-0303459P.
Predicting of effects by control of the exposed to the tissues or of the exposed to the exposed 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat sequence differentially expressed in response to a hepatotoxin #1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or set invalidation of other intracellular hormone receptors. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2000; 2000US-0222040P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK63701 standard; cDNA; 1500
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                                                                                                                                                                                                                                                                                                                                                                  (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                        2002-241625/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatotoxin;
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                             toxic effects of compounds or the progression of these toxic determining the changes in gene expression in tissues or cells the toxin and comparing these to gene expression in unexposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.1%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                               Porter MW,
                                                                                                                                                                                                                                                                                                                                                              LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence tag; EST; drug screening; on; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                               Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                               Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 1.2e-21;
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                                                                                                                                                                                                                                                                               Elashoff MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Claim 1;

SEQ ID NO 1608; 239pp; English

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RESULT 8
ADB58201
ID XXX ACC XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC expression in a tissue or cell sample exposed to the compound of two or common genes listed in the specification, where differential expression of CC the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates in a CC cell. The methods utilise a set of at least two probes (on a solid CC support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer CC system comprising at database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a Set of genes comprising at least two genes listed in the specification, and computer CC cand a user interface to view the information used to present information CC insted in the specification. The method is useful for elucidating global CC changes in gene expression and for identifying toxicity markers in CC cissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and CC gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 77
                           31-JAN-2002;
15-MAR-2002;
15-MAR-2002;
30-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          grug
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                                                                                                                                                                                          31-JAN-2003;
                                                                                                                                                                                                                                                                07-AUG-2003
                                                                                                                                                                                                                                                                                                                              WO2003064624-A2
                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toxic; toxin; gene expression profile; hepatotoxicity; liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxicity-related gene, SEQ ID 3227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                          screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299
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                           2002US-00060087.
2002US-0364045P.
2002US-0364055P.
2002US-0436643P.
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                                                                                                                                                                                              2003WO-US003194
                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxicity assay; ds
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98.7%;
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Pred. No. 3.
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Mismatches 1
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RESULT 9
ADB52710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for predicting a toxic effect CC of a compound. The method comprises preparing a gene expression profile CC of a tissue or cell sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 1-4925, where CC The method is useful for predicting at least one toxic effect. The method is useful for predicting at least one toxic effect. CC The method redicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the least one activity of a protein The method and compositions of the CC differential expression, are useful in identifying toxicity markers in CC differential expression, are useful in identifying toxicity markers in CC differential expression, are useful in identifying toxicity sassys. Note: The sequence data for this patent did not form part of the printed consecutive that provided the component of the printed consecutive to the printed consecutive t
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Best Local S
Matches 77
08-APR-2002;
10-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                                                                       toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
                                                             04-FEB-2002;
13-MAR-2002;
                                                                                                                            04-FEB-2003;
                                                                                                                                                                   14-AUG-2003
                                                                                                                                                                                                             WO2003065993-A2
                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                          Primary rat hepatocyte toxicity modelling related gene
                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA; 1500
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                   2002US-0353171P.
2002US-0363534P.
2002US-0370248P.
2002US-0371134P.
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                                                                                                                          2003WO-US003482.
  2002US-0371135P
                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 A; 408
                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
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Pred. No. 3.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Higgs
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3.2e-13;
hes 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other;
                                                                                                                                                                                                                                                                                                                                  diagnostic marker
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:3252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298
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RESULT 10
ABT41911
ID ABT41
XX ABT41
XX ABT41
XX TOXIC
DT 26-JU
XX TOXIC
XX TOXIC
XX TOXIC
XX TOXIC
XX TOXIC
XX ABT41
XX TOXIC

modelling

related

rat gene SEQ ID No 1613

26-JUN-2003 ABT41911,

(first entry)

ABT41911 standard;

DNA; 1500

ВP

Rattus norvegicus

Toxic effect; gene expression profile; renal toxicity; database; drug screening; toxicity assay; rat; ds.

toxicity marker;

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                                                                                                                                                                       Matches
                                                                                                                            Query Match
Best Local
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11-APR-2002;
19-APR-2002;
19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                            preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                     Sequence 1500 BP; 336 A; 408 C; 380 G;
                                                                                                                                                                                                                                                                                                                                                                            compound induces
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-731472/69
                                                                                                                                                                                                                                                                                                                                                                                        The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mean values.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENE-)
                                                                                                                            Local Similarity
                            299
                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                    44; SEQ ID NO 3252; 874pp; English
8
                                                                                                               77;
                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENE
                  CACTTCCGCTACTAGCTA 316
                                                                         CACTICCGCTACTATCTA 85
                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z (U
                                                                                                                                                                                                                                                                                                                                                                                           invention
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2002US-0373613P.
2002US-0373602P.
2002US-0373602P.
2002US-0374139P.
2002US-037853P.
2002US-0378653P.
2002US-0378655P.
                                                                                                               Conservative
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2002US-0407688P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002US-0394230P
                                                                                                                                                                                                                                                                                                                                                                         ntion describes a method for determining whether a a toxic effect on a tissue or cell. The method comprises
                                                                                                                           23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson
                                                                                                               <u>,</u>
                                                                                                                            Score 76.4;
Pred. No. 3.
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                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higgs
                                                                                                                                                                       376 T;
                                                                                                                         DB 10;
1.2e-13;
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                                                                                                               1;
                                                                                                                                                                       0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Castle A,
                                                                                                               Indels
                                                                                                                                          Length
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WO200295000-A2

2001US-0292335P 2002WO-US016173

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Best Local :
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10-JUL-2001; 2001US-0303807P.
10-JUL-2001; 2001US-0303807P.
10-JUL-2001; 2001US-0303810P.
28-AUG-2001; 2001US-0333810P.
27-SEP-2001; 2001US-0334928P.
27-OCT-2001; 2001US-0334928P.
27-OCT-2001; 2001US-0334928P.
27-OCT-2001; 2001US-0331805P.
27-OCT-2001; 2001US-0338144P.
27-PEB-2002; 2002US-0357842P.
27-PEB-2002; 2002US-0357843P.
27-PEB-2002; 2002US-0357844P.
28-APR-2002; 2002US-0357844P.
29-APR-2002; 2002US-0357844P.
20-APR-2002; 2002US-0370144P.
20-APR-2002; 2002US-0370144P.
20-APR-2002; 2002US-0370144P.
                                                                                                                                                                                                                 information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxic. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polymucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2001;
13-JUN-2001;
19-JUN-2001;
                                                                                                                                                                             Sequence 1500 BP; 336 A; 408
                                                                                                                                                                                                        Organization
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel method of predicting at least one toxic effect of a compound. The method compurises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page; 446pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 profile to a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Predicting at least one toxic effect of a compound, useful i modeling, comprises preparing a gene expression profile of a cell sample exposed to the compound, and comparing the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-2002;
17-APR-2002;
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                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-148464/14.
                            299
                                                                                       239
 68
                                                                                                                  77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENE
                                                                                                                                   Similarity
                                                                      CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                            CACTICCGCTACTAGCTA 316
CACTTCCGCTACTATCTA 85
                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0371679P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0370247P
2002US-0372794P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porter M,
                                                                                                                              23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson
                                                                                                                Score 76.4; DI
Pred. No. 3.2e
0; Mismatches
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                                                                                                                                                                             C; 380
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.2e-13;
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                                                                                                                  Indels
                                                                                                                                              Length 1500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for toxicity a tissue or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression
                                                                                                                Gaps
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239 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 298

Query Match Best Local S Matches 77

l Similarity 77; Conser

23.8%;

Score 76.4; I Pred. No. 3.2e 0; Mismatches

.4; DB 12; 3.2e-13;

Length 1500; Indels

0

Gaps

0 Other;

Sequence 1500

BP; 336 A; 408 C; 380 G; 376 T; 0 U;

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RESULT 11
ADP72689
ID ADP72
CC The invention relates to a method of predicting (the progression of) a CC toxic effect of a compound by preparing a gene expression profile of a CC kidney tissue or cell sample exposed to the compound and comparing the CC gene expression profile to a database, or detecting the level of gene (s) CC expression in a tissue or cell sample exposed to the compound, where CC differential gene expression compared to a control indicates a toxic ceffect (toxicity progression). The method is useful for predicting (the CC progression of) at least one toxic effect of a compound. The genes are CC methods are useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as mephritis, CC kidney necrosis, glomerular and tubular injury, or focal segmental CC glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for CC predicting or elucidating the potential cellular pathways influenced, CC induced or modelling the toxic response of a test compound, for CC method of the progression of renal disease states, for identifying genes CC that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the CC method of the invention. (Note: The sequence data for this patent did not CC form part of the printed specification, but was obtained in electronic CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differential gene expression; toxicity progression; toxicity marker; drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; toxic ci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-460771/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-2002; 2002US-00301856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-2003; 2003WO-US037556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Renal toxin progression gene marker #1278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxic effect;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 1278; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression profile; kidney tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KR, Castle
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                                                                                                                                                                                                             The present invention describes a method of screening a test agent for chepatotoxicity. The method comprises: (a) providing a test cell population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKWARKER 1-8 and INJURYMARKER 1-10; (b) contacting the test cell population with a test agent; (c) measuring expression of one or more of the nucleic acid sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression of the nucleic acid sequence in an reference cell population comprising at least one cell whose exposure status to a hepatotoxic agent in known; and (e) identifying a difference in expression levels of the RISKWARKER cor INJURYMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification of the present invention and part of the present invention.
                                                                                                            Matches
                                                                                                                                       Query Match
                                                                                                                                                                     Sequence 5001 BP; 1225 A; 1204 C; 1261 G; 1311 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 22-24; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-355948/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gould-Rothberg BE,
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20-NOV-2000;
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                                                                                                                                                                                                     present
                                                                                                                         Similarity
                                                                CACTICCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTICCGCTACTATCTA 85
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Conservative
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                                                                                                                                                                                                       invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dipippo VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                       23.8%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hepatotoxic; differential gene expression; NSAID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5001
                                                                                                          0;
                                                                                                         Score 76.4; DB 4;
Pred. No. 4.7e-13;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramseh TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerwein
                                                                                                                                    Length 5001;
                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression
                                                                                                         Gaps
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RESULT 13
ABN95896
ID ABN95
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                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel method for diagnosing and detecting the compression of liver cancer, hepatocellular carcinoma or metastatic liver curve thepatocellular carcinoma in a patient, and differentiating metastatic liver cancer from thepatocellular carcinoma in a patient, involving detecting the level of the expression of two or more genes represented in ARN93503-ARN97455 in a crisque sample. The method of the invention has hepatotropic, and crisque sample the entire that is useful for diagnosting and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, charters that can be used to monitor disease states, disease progression, charters that can be used to monitor disease states, disease progression, charters that can be used to monitor disease states, disease progression, charters that can be used to monitor disease states, disease progression, control the printed specification, but was contained in electronic format directly from WIPO at
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                            Sequence 6128 BP; 1504 A; 1497 C; 1504 G; 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2394; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horne D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2000; 2000US-0237054P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2001; 2001WO-US030589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene #2394 used to diagnose liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN95896 standard; DNA; 6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENE LOGIC INC
                                                                            498
                                                                                                                 129
                                                                                                                                                       438
                                                                                                                                                                                                                               156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CACTTCCGCTACTATCTA 78
CCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGCGAGCATCGGCCACCGCCATCC----
                                  AGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGA
                                                                            ACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCATTAACCTCCTGGTGCAAGTGGCGCGCG
                                                                                                              ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC-----
                                                                                                                                                       Alvares C,
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                  19.9%;
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                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                               Score 63.8; DB 6;
Pred. No. 3.9e-09;
0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                                                                                                                                                                                                                                                            T; 0 U; 0 Other
                                                                                                                                                                                                                                                                    Length 6128;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                    19;
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RESULT 14
ABV75371
ID ABV75
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            Detecting the presence or diagnosing the risk of a liver cancer patient comprises detecting aborrant expression of a gene encodi
                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2003
                                                                                                         03-MAY-2001; 2001US-0288441P
                                                                                                                       03-MAY-2002; 2002WO-AU000558
                                                                                                                                                      WO200290580-A1
                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                Human IGFBP-1 gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV75371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABV75371
     insulin-like growth
                                                           Huynh TH,
                                                                         (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
(SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.
(ARGA/) ARGAET V P.
                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                          cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                               Insulin-like growth factor binding protein; IGFBP; cytostatic; liver;
                                    P-PSDB;
                                                                                                                                                                                                                                                                                                        intron
                                           2003-103522/09
                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614
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                                    ABB82757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCACTTC 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CATCCAGCGAGCATCTGCCGCCGCCGCCGCCGCCACCCTCCCAGAGAGCACTGGCCA 669
                                                           Chow PKH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (firet
                                                                                                                                                                                                                                                                                                                                                                                                          IGFBP-1;
                                                                                                                                                                                                                                      /rcag= e
/number= 2
                                                                                                                                                                                           /*tag= g
/number= 3
                                                                                                                                                                                     5069.
                                                                                                                                                                                                                                                                       2657. .2826
/*tag= d
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762. .5200
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                                                                                                                                                                                                                                                                                                              'number= 1
                                                                                                                                                                                                                                                                                                                                    ontains
                                                                                                                                                                                                                   number= 3
                                                                                                                                                                                                                                                                                                                                        product= "IGFBP-1"
note= "insulin-like growth factor binding protein;
                                                                                                                                                                                                          170. .5068
                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                         827. .4040
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     factor binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver; uterus; ovary; stomach; metabolic disease; developmenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to detecting the presence or diagnosing the risk of a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGBBP). The method is useful for detecting the presence or diagnosing the risk of a method is useful for detecting the presence or diagnosing the risk of a
                                                                                                                                                                                                                                                                                04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tissue specific; diagnosis; brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human liver cell specific cDNA sequence SEQ ID NO:329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGFBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
                                                                                                           WPI; 2001-291057/30
                                                                                                                                                                  Sornasse
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                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200132927-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective;
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                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 104-108; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CATCCAGCGAGCATCTGCCGCCGCGCCGCCGCCACCCTCCCAGAGAGCACTGGCCA
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                                                                                                                                                                                                                                                                                99US-0163508P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vary; stomach; intestine; kidney; pancreas; ss;
e; developmental disease; cytostatic; immunomodulatory;
gene therapy; cancer; immunopathology; neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA;
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Pred. No. 3.9e-09;
0; Mismatches 72
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New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology.

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CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide CC sequences (I). (I) can have cytostatic, immunomodulatory and CC neuroprotective activities, and can be used in gene therapy. (I) and CC proteins (II) encoded by then are used in high throughput screening CC assays to select DNA molecules, RNA molecules, peptide nucleic acids, CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical CC agents. Expression of (I) in a sample indicates the differentiation of CC embryonic stem cells into a tissue selected from brain, heart, kidney, CC liver, lung, skeletal muscle or pancreatic tissues (I) and (II) are used CC developmental process, treatment, condition, disease or disorder. The CC gene profile can be used for diagnosis, prognosis or monitoring of CC treatments and for investigating a predisposition to a disorder where the GC gene is associated with a cancer, immunopathology or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.9
Best Local Similarity 63.2
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6134 BP; 1505 A; 1498 C; 1507 G; 1624 T; 0 U; 0 Other;
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670
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                                                                                                                     614 ----CATCCAGCGAGCATCTGCCGCCGCCGCCGCCACCCTCCCAGAGAGCACTGGCCA
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CCGCTCC 676
                                                      CCACTTC 304
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Pred. No. 3.9e-09;
0; Mismatches 72;
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Search completed: September 1, Job time: 342.384 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13.7	14.8	14.8	14.8	14.8	17.2	17.2	17.2	20.5	20.5	20.5	20.5	20.5	20.5	41.4	58.9	59.0	60.1	86.3	100.0	Query Match
51	13011	13011	13011	194	6134	6128	6128	5001	1500	1500	1500	1500	1500	423	219	270	423	321	372	% Query Match Length
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ABX15380	ADP72914	ABT42448	AAT96631	AAT43002	AAH57489	ABV75371	ABN95896	AAH22429	ADP72689	ABT41911	ADB52710	ADB58201	ABK63701	ABX15376	ABX15372	ABX15373	ABX15376	ABX15374	ABX15375	ID
Abx15380 Rat liver	Adp72914 Renal tox	Abt42448 Toxicity	Aat96631 cDNA enco	Aat43002 Rat type	Aah57489 Human liv	Abv75371 Human IGF	Abn95896 Gene #239	Aah22429 Rat insul	Adp72689 Renal tox	Abt41911 Toxicity		×	Abk63701 Rat seque			•	Abx15376 Rat ingul	Abx15374 Rat insul	Abx15375 Rat insul	Description

The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene

Claim 9; Page 14; 37pp; English.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in liver cells.

WPI; 2002-674190/72.

C 45						c 39		37	36		c 34			31	30			c 27			24		c 22	
34	34	34	34	34	34	35	35.6		35.8			36.6	36.8	. 37	37.4	37.6	37.6		37.8			48	51	. 51
9.1	9.1	9.1	9.1	9.1	9.1	9.4	9.6	9.6	9.6	9.7	9.8	9.8	9.9	9.9	10.1	10.1	10.1	10.2	10.2	10.2	10.4	12.9	13.7	13.7
10543	10543	10537	10537	10537	10537	3895	490	11009	11009	586	3054	1678	761	3896	12850	3191	1254	7061	7061	7061	44861	48	270	51
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AAK69583	AAS35770	ADJ07881	ADE46463	AAK69582	AAS35769	ABN87725	ACH34858	AAI70816	ABQ72907	ACH71991	ABS70481	ADA52441	ABL90266	ADQ64446	ADB36326	ACH87111	AAS77024	AAS61189	ABL70248	ABL32997	AAS20000	ABX15379	ABX15373	ABX15371
Aak69583 Human imm	Aas35770 Human car	Adj07881 Human car	Ade46463 Human car		Aas35769 Human car	Abn87725 Human pro	Ach34858 Human end		Abq72907 Mouse lam	Ach71991 Human gen	Abs70481 Human bon	Ada52441 Human cod	Abl90266 Human pol	Adg64446 Novel hum	Adb36326 Human fac	Ach87111 Human gen	Aas77024 DNA encod	Aas61189 Human gen	Abl70248 Chemicall	Abl32997 Human imm	Aas20000 DNA encod	Abx15379 Rat liver	Abx15373 Rat insul	Abx15371 Rat gluco

ALIGNMENTS

ABX15375;

ABX15375 standard; DNA; 372 BP.

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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                  11-OCT-2000; 2000US-0239113P.
                                                                                                                                                                                       10-OCT-2001; 2001US-00972916.
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                                                                                                                                                                                                                                     US2002107198-A1
                                                                                                                                                                                                                                                                    Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2003
                                                                                                                                                                                                                                                                                           intracellular hormone receptor; insulin regulator construct; anabolic
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RESULT 2
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Best Local
                                                                                                                                                 Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-: insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; protein catabolism; protein degradation; antidiabetic; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat insulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABX15374
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                                                                                                                             intracellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                   regulator construct DNA #2.
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                                                                                                                        TOTINOTE
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Pred. No. 6.8e-103;
); Mismatches 0;
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                                                                                                                        construct; anabolic
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Synthetic Rattus norvegicus

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Best Local Similarity
Matches 321; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insu
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301
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                                                                                                                                                                                                                                                                      CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                                                                                                                          TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGTGCTGCCGAG
 CTTCCGCTACTAGCTAGCCGC
                             CTTCCGCTACTAGCTAGCCGC
                                                                  CAAACCCAGCGAGCATTGAACACTGCACACGCCATCTGCCCAGAGAGCTGTGACCACCA
                                                                                                                                   CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                                                                                                   TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCCGTGCTGCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin
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                                                                                                                                                                                                                                                                                                                                                                                                                       86.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 321; DB 6;
Pred. No. 2e-87;
                                 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 321;
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                                                                                                                                                     Query Match
Best Local S
Matches 297
                                                                                                                                                                                                                                Sequence 423 BP; 81 A; 149 C; 116 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-: Insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 14; 37pp; English.
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                                                                                                                                                                                                                                                                 inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequences a rat insulin regulator construct of the invention
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  94
                                    62
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                                                                                                                 N
                                                                                                                                                                          Similarity
CCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA
                                  GCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGGGCCCAGAGTC
                                                                        ACTOTOGCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCC
                                                                                                             ACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGG
                                                                                                                                                       Conservative
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                                                                                                                                                                        60.1%;
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                                                                                                                                                                        Score 223.6;
Pred. No. 8.8
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                                                                                                                                                                                                                                77 T; 0 U; 0 Other;
                                                                                                                                                                          .8e-58;
                                                                                                                                                                                            DB 6;
                                                                                                                                                     74;
                                                                                                                                                     Indels
                                                                                                                                                                                          Length 423;
                                                                                                                                                                                                                                                                                       This sequence
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRS) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISB) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucosorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1 insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; callular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                                                                                                                                             New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insuliver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                          9; Page
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insulin;
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Matches 220
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                                                                                                                                                                                                                                                                                                                                          Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP: insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulininsulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; hepatoma; cellular protein degradation; antidiabetic;
                                                                     New insulin regulator cassette, useful e.g. for treating diabetes
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                                                       specific,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTAGCCGC 372
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                                                                                                                                                                                     2000US-0239113P
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                                                       glucose-inducible transgenic
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                                                                                                                                                                                                                                                                                                                               receptor;
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Pred. No. 1.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 G; 47 T; 0 U; 0 Other;
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                                                       expression
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                                                         of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                                                                                                                                                                                                                                                                                                                                                                     insulin;
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Claim

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13;

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RESULT 6
ABX153
XX ABX153

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin-sensitive element of the invention
                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat insulin regulator construct DNA #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX15376
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                                                                   11-OCT-2000; 2000US-0239113P
                                                                                                                                       10-OCT-2001; 2001US-00972916.
                                                                                                                                                                                                                                                                               US2002107198-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       intracellular hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 57 A; 77 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor; insulin regulator construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 1.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 G; 37 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           anabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other catbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, or inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
 31-JUL-2000; 2000US-0222040P
02-NOV-2000; 2000US-0244880P
                                                     30-JUL-2001; 2001WO-US023872
                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                  Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
                                                                                                                                                                                                                                                   Rat sequence differentially expressed in response to a hepatotoxin #1608
                                                                                                                                                                                                                                                                                                                                ABK63701;
                                                                                                                                                                                                                                                                                                                                                                 ABK63701 standard; cDNA; 1500 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 423 BP; 81 A; 149 C; 116 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGRBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                           WO200210453-A2
                                                                                                                                                                                                                                                                                            18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents a rat insulin regulator construct of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thule PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGGAACCACGGGAGTGCCCCGTGCGCCCCATGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGGGCCAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGGGCCCAGAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 100.0%;
Conservative (
                                                                                                                                                                                                 expression; centrilobular
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 154; DB 6; Pred. No. 1.2e-36;
                                                                                                                                                                                               necrosis; steatosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 8
ADB58201
ID ADB5
XX
AC ADB5
XX

ADB58201 standard;

DNA;

1500

ВP

ADB58201

S 밁 á

68

CACTTCCGCTACTATCTA

85

350 CACTTCCGCTACTAGCTA 367

œ

290 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCCTGTGACCAC 349

CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC 67

Matches

77;

Conservative

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Query Match Best Local Similarity

20.5%;

Score 76.4; Pred. No. 76 Mismatches

7e-13; BB 6 1;

Length 1500; Indels

0

Gaps

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CC cells. Also included are methods of predicting at least one toxic effect
CC of a compound or progression of a toxic effect, preferably the
CC hepatotoxicity of a compound, comprising detecting the level of
CC hepatotoxicity of a compound, comprising detecting the level of
CC expression in a tissue or cell sample exposed to the compound of two or
CC more genes listed in the specification, where differential expression of
CC the genes is indicative of at least one toxic effect or progression. The
CC method can also be used to identify an agent which modulates the toxic
CC response and predict cellular pathways that a compound modulates in a
CC cell. The methods utilise a set of at least two probes (on a solid
CC support in kit form), where each of the probes comprises a sequence that
CC specifically hybridises to a gene listed in the specification, a computer
CC system comprising at database containing information identifying the
CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
CC set of genes comprising at least two genes listed in the specification,
CC and a user interface to view the information used to present information
CC listed in the specification. The method is useful for elucidating global
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                           toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or ce sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or
Sequence 1500 BP; 336 A; 408 C; 380 G;
                                                                                                                                                                                                                  changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to methods for predicting toxic effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-241625/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-2001;
19-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1608; 239pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0290029P.
2001US-0290645P.
2001US-0292336P.
2001US-0295798P.
2001US-02957457P.
2001US-0298884P.
2001US-0303459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castle AL,
376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elashoff MR;
                                                                      from a gene
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04-DEC-2003

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RESULT 9
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ID ADB5
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AC ADB5
XX
AC ADB5
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OT 04-E
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                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method for predicting a toxic effect CC of a compound. The method comprises preparing a gene expression profile CC of a tissue or cell sample exposed to the compound, and comparing the CC gene expression profile to a database comprising SEQ ID 1-4925, where CC gene expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the CC present invention using a database of genes having liver toxin-induced CC differential expression, are useful in identifying toxicity markers in CC liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed compositions of the printed to the printed t
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug
    04-DEC-2003
                                           ADB52710;
                                                                                 ADB52710 standard; DNA; 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2002; 2002US-00060087.
15-MAR-2002; 2002US-0364045P.
15-MAR-2002; 2002US-036405SP.
30-DEC-2002; 2002US-0436643P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxicity-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JAN-2003; 2003WO-US003194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                    CACTTCCGCTACTAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1500
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                                                                                                                                                                                                                                                                                                                                                               Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxicity assay; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                336 A; 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression profile;
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                                                                                                                                                                                                                                                                                                                                                                                20.5%;
98.7%;
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                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                Score 76.4; DB 10;
Pred. No. 7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 380
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                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatotoxicity;
                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 1500;
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22-APR-2002;
08-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxicity marker; toxicity progression; drug screening primary rat hepatocyte toxicity modelling; gene; ds
WPI; 2003-731472/69
                           Mendrick D,
Elashoff M;
                                                                                                                               09-JUL-2002;
                                                                                                                                                            09-MAY-2002;
                                                                                                                                                                                                                                 19-APR-2002;
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11-APR-2002;
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13-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxic effect; gene expression profile; toxicity marker; toxicity progression;
                                                                                                                                                                                                                                                                                            10-APR-2002;
                                                                                                                                                                                                                                                                                                          10-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primary rat hepatocyte toxicity modelling
                                                                       (GENE-)
                                                                      GENE
                                                                                                                                                                                      2002US-0371150P
2002US-0371413P
2002US-0373601P
2002US-0373602P
2002US-0378370P
2002US-0378370P
2002US-0378370P
2002US-0378370P
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2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
                                                                                                                 2002US-0394253P
2002US-0407688P
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                                                                      LOGIC INC
                                                                                                   2003US-0442900P
                                                                                                                                               2002US-0394230P
                                                                                                                                                            2002US-0378653P
2002US-0378665P
                                          Porter M,
                                                                                                                                                                                                                                                                                                                                                      2002US-0353171P
                                          Johnson
                                         ۲
                                          Higgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatotoxicity;
drug screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related gene
                                          Castle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic marker;
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Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.

Claim 44; SEQ ID NO 3252; 874pp; English

genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The toxicity modelling related gene sequence from the present invention

Sequence 1500 B₽; 336 A; 408 Ç 380 ç, 376 T; 0 U; 0 Other;

밁 S Matches Query Match Best Local : 290 æ . Similarity 77; Conserv CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 20.5%; 98.7%; Score 76.4; I Pred. No. 7e-1 0; Mismatches 0; 4; DB 10; 7e-13; 1; 0, Gaps 67

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ARBULT ABBULT ARBULT AR
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10-JUL-2001; 2001US-0303807P

10-JUL-2001; 2001US-0303807P

10-JUL-2001; 2001US-0303810P

28-AUG-2001; 2001US-0319462P

27-SEP-2001; 2001US-0330462P

01-NOV-2001; 2001US-0330462P

01-NOV-2001; 2001US-0331805P

21-NOV-2001; 2001US-03318044P

19-DEC-2001; 2001US-03318044P

19-DEC-2001; 2001US-0336144P

19-DEC-2001; 2001US-0336144P

19-DEC-2001; 2002US-0357843P

21-FEB-2002; 2002US-0357844P

15-MAR-2002; 2002US-0357844P

16-APR-2002; 2002US-0357044P

08-APR-2002; 2002US-0370144P

08-APR-2002; 2002US-0370144P

08-APR-2002; 2002US-0370206P

08-APR-2002; 2002US-0370206P

08-APR-2002; 2002US-0370209P

17-APR-2002; 2002US-0370294P

21-APR-2002; 2002US-0370299P
The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxicity markers in as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                     Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2001;
13-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                       Example 4; Page; 446pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porter
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screening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Α,
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Elashoff

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glomerular

tubular injury, or focal

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RESULT 11
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ID ADP72689
ID ADP72689
ID ADP72
XX ADP72
XX ADP72
XX ADP72
XX AG; t
KW diffe
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XX Focall
XX Focal
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Best Local
                 The invention relates to a method of predicting (the progression of) a toxic effect of a compound by preparing a gene expression profile of a kidney tissue or cell sample exposed to the compound and comparing the gene expression profile to a database, or detecting the level of gene (s) expression in a tissue or cell sample exposed to the compound, where differential gene expression compared to a control indicates a toxic effect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The methods are useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis,
                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 1278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predicting (the progression of) a toxic effect of a compound, monitoring the progression of renal disease states, comprises gene expression profile of a kidney tissue or cell sample exports.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; toxic effect; gene expression profile; kidney tissue; differential gene expression; toxicity progression; toxicity drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represents a rat DNA sequence relating to the toxic effect databate described in the specification. NOTE: The sequence data for this did not form part of the printed specification, but was obtained electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-460771/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-2003; 2003WO-US037556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP72689
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98.7%;
                                                                                                                                                                                                                                                                                                                                                                   266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson KR,
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The present invention describes a method of screening a test agent for hepatotoxicity. The method comprises: (a) providing a test cell population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKMARKER 1-8 and INJURYMARKER 1-10; (b) contacting the test cell population with a test agent; (c) measuring expression of one or more of the nucleic acid sequences in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population; (d) comparing the expression of the nucleic acid sequence in the test cell population to the expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1999;
18-FEB-2000;
20-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a toxic response to one or more individual compounds and for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent. The kit is useful for predicting or modelling the toxic response of a test compound, for monitoring the progression of renal disease states, for identifying genes that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the method of the invention. (Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                 Screening hepatotoxic agent comprises contacting test cell population expressing RISKMARKER or INJURYMARKER with agent, comparing expression with reference population and identifying difference in expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gould-Rothberg BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2000; 2000WO-US032049.
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Best Local
tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN9303-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at least one cell whose exposure status to a hepatotoxic agent in known and (e) identifying a difference in expression levels of the RISKMARKER or INJURYMARKER sequences, if present, in the test cell population and reference cell population. The method is useful for identifying a hepatotoxic agent. The present sequence is given in the exemplification
                                                                                                                                                                                                                                                                                               Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene, liver cancer, ds, hepatocellular carcinoma, hepatotropic, metastatic liver tumour, cytostatic, expression profile. Ainco
                                                                                                                                                                                                           The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver
                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2394; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-426119/45.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                    Human IGFBP-1
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WO200290580-A1
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/number= 2
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Pred. No. 7.3e-09;
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RESULT 15
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XX IO-SE
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Matches 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to detecting the presence or diagnosing the risk of a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (IGFBP). The method is useful for detecting the presence or diagnosing the risk of a liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGFBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
                                                                                                                           AAH57489;
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                                                                                                10-SEP-2001
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DB; ABB82757.
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                                                                                                                                                      standard; cDNA; 6134
                                                                                                                                                                                                                          CCGCTCC 676
                                                                                                                                                                                                                                                      CCACTTC 355
                                                                                                                                                                                                                                                                                ----CATCCAGCGAGCATCTGCCGCCGCCGCCGCCACCCTCCCAGAGAGCACTGGCCA
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Pred. No. 7.3e-09;
"" matches 72;
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Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss; metabolic disease; developmental disease; cytostatic; immunomodulatory;

heart; skeletal muscle;

Human liver cell specific cDNA sequence SEQ ID NO:329

neuroprotective;

gene therapy; cancer;

immunopathology; neuropathology

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC AAH57161 to AAH57576 represent cell and tissue specific polynucleotide CC sequences (I). (I) can have cytostatic, immunomodulatory and concern sequences (I) can have cytostatic, immunomodulatory and CC neuroprotective activities, and can be used in gene therapy. (I) and CC proteins (II) encoded by then are used in high throughput screening contents of the periode sequences. RNA molecules, peptide nucleic acids, minetics, peptides, proteins, agonists, antagonists, antibodies or their contents, inmunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of combronic stem cells into a tissue selected from brain, heart, kidney, cliver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The conditions are used for treatments and for investigating a predisposition to a disorder where the gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene profile can be used for investigating a predisposition or neuropathology
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.2
Best Local Similarity 63.2
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6134 BP; 1505 A; 1498 C; 1507 G; 1624 T; 0 U; 0 Other;
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Search completed: September Job time: 396.464 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adp72914 Renal tox	ADP72914	12	13011	13.0	55.2	20	
Abt42448 Toxicity	ABT42448	10	13011	13.0	55.2	19	
Aat96631 cDNA enco	AAT96631	N	13011	13.0	55.2	18	
Aat43002 Rat type	AAT43002	N	194	13.0	55.2	17	
Aah57489 Human liv	AAH57489	4	6134	14.4	60.8	16	
Abv75371 Human IGF	ABV75371	10	6128	14.4	60.8	15	
Abn95896 Gene #239	ABN95896	თ	6128	14.4	60.8	14	
Aah22429 Rat insul	AAH22429	4	5001	18.1	76.4	13	
Adp72689 Renal tox	ADP72689	12	1500	18.1	76.4	12	
	ABT41911	10	1500		76.4	11	
Adb52710 Primary r	ADB52710	10	1500	18.1	76.4	10	
Adb58201 Toxicity-	ADB58201	10	1500	18.1	76.4	9	
Abk63701 Rat seque	ABK63701	σ	1500	18.1	76.4	8	
Abx15374 Rat insul	ABX15374	9	321	24.3	103	c 7	
Abx15375 Rat insul	ABX15375	σ	372	36.4	154	6	
Abx15372 Rat insul	ABX15372	σ	219	51.8	219	5	
Abx15374 Rat insul	ABX15374	9	321	51.9	219.4	4	
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Abx15373 Rat insul	ABX15373	σ	270	63.8	270	N	
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8.9	8.9	8.9	8.9	8.9	8.9	8.9	8.9	9.1	9.1	9.6	9.6	9.6	9.7	9.7	10.1	10.5	10.8	10.9	11.0	11.3	11.4	12.0	12.1	12.1
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ADJ30178	ABX59428	AAL36440	AAS61189	ABL70248	ABL32997	ABQ54073	ABQ54072	AAI70816	ABQ72907	ADH57071	ADH62916	ADD00956	ABQ54068	ABQ54069	ABX15376	AAS77024	ACH71991	ADB36326	ADQ64446	ABX15379	ACH87111	AAS20000	ABX15371	ABX15380
Adj30178 Human mus	Abx59428 cDNA enco	Aal36440 Human mus	Aas61189 Human gen	Ab170248 Chemicall		Abq54073 Oligonucl	Abq54072 Oligonucl	Aai70816 Mouse lam	Abq72907 Mouse lam	Adh57071 Genomic h	Adh62916 Human Jag	Add00956 Human Jag	Abq54068 Oligonucl	Abq54069 Oligonucl		Aas77024 DNA encod	Ach71991 Human gen	Adb36326 Human fac	Adq64446 Novel hum	Abx15379 Rat liver	Ach87111 Human gen	Aas20000 DNA encod	Abx15371 Rat gluco	Abx15380 Rat liver

ALIGNMENTS

17-APR-2003

(first entry)

ABX15376 standard; DNA; 423

ВP

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Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; catabohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anabolic.
                                                                                                         WPI; 2002-674190/72.
                                                                                                                                                                                                       10-OCT-2001; 2001US-00972916.
                                                                                                                                                                                                                                 08-AUG-2002.
                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                          Rattus norvegicus.
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                                                                                                                                                        (THUL/) THULE P M.
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene

Claim 9; Page 14; 37pp; English.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in liver cells.

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RESULT 2
ABX15373
ID ABX1
XX ABX1
AC ABX1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabblism and to retard protein catabblism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may
                                                                                                                                                                                                                                                                                                                                                                                                                                                      inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like gra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insuliver cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             have effects additional to those provided by secreted insulin, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 13-14; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                   270;
241
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                                                                   181
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                                                                                                                                                                                                                                                                                                   CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA 213
                      TGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                             AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
                                                                                                                                                                                                                                                                                 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA
                                                                   GCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG
                                                                                                      GCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG
                                                                                                                                         AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                         270 BP; 63 A; 95 C; 65 G; 47 T; 0 U; 0 Other;
TGACCACCACTTCCGCTACTAGCTAGCCGC
                                                                                                                                                                                                                                                                                                                                                       Conservative
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М.
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Pred. No. 1.6e-73;
0; Mismatches 0;
270
                                                                                                                                                                                                                                                                                                                                                                                      Length 270;
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ABX15375

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                                                                                                                                              Query Match
Best Local S
Matches 297
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                                                                                                                                                                                                                  Sequence 372 BP; 87 A; 128 C; 102 G; 55 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Page 14; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
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Synthetic.
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GCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGGGCCAGAGTC
                                cccaereracareececaceeeecacreccereerrecreeacrereecececeaerera 153
                                                                                                        ACTCTGGCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCC
                                                                      ACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGG
                                                                                                                                                Conservative
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                                                                                                                                                               52.9%;
76.2%;
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                                                                                                                                                               Score 223.6;
Pred. No. 4.3
                                                                                                                                              Mismatches
                                                                                                                                                               4.3e-59
                                                                                                                                                                                DB 6;
                                                                                                                                            74;
                                                                                                                                              Indels
                                                                                                                                                                              Length 372;
                                                                                                                                              19;
                                                                                                                                          Gape
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RESULT 4
ABX15374
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            The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other carbohydrates) and glucocorticoids and inhibition by glucagon so that a
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                                                                                                                                                                                                                     New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.
carbohydrates) and glucocorticoids and inh combination of these effects can maintain
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RESULT 5
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Best Local S
Matches 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                       New insulin regulator cassette, useful e.g. for treating diabetes provides specific, glucose-inducible transgenic expression of insulver cells.
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                                                                                                                                                                                                                                                                                            norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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                                                                                                                                                                                                                                                                                                                     receptor;
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Pred. No. 8.2
                                                                                                                                                                                                                                                                                                                        insulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                     regulator construct; anabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2e-58;
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                                                    expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other;
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                                                                                                                                                                                                                                                                                                                                                                                          IGFBP-1;
insulin;
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Claim

8

Page

13;

37pp; English

(THUL/) THULE P M

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RESULT 6
ABX15375/c
ID ABX153
XX ABX153
XX ABX153
XX ABX153
XX Glucos
KW Glucos
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Best Local Similarity
Matches 219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carabohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                 11-OCT-2000; 2000US-0239113P
                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat insulin regulator construct DNA #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-2003
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                                                                                                                                   10-OCT-2001; 2001US-00972916.
                                                                                                                                                                                                                                                                          US2002107198-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatocyte; hepatoma;
intracellular hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor; insulin regulator construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 C; 48 G; 37 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372
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                                                                                                                                                                                                                                                                                                                                                                                                                                          anabolic
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RESULT 7
ABX15374/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used CC to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties CC thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-cc differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. Charletton of cellular protein degradation, and inhibition, or CC stimulation of other intracellular hormone receptors. This sequence corporesents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                    Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1 insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulir insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat; glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                US2002107198-A1
                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                    Rat insulin regulator construct DNA #2.
                                                                                                                                                                                                                                                                                                             17-APR-2003
                                                                                                                                                                                                                                                                                                                                                  ABX15374;
                                                                                                                                                                                                                                                                                                                                                                                        ABX15374 standard; DNA; 321 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an insulin regulator construct comprising glucose response element (GIRE) of a liver pyruvate kinase (LPK) go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin liver cells.
                                                                                                                intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thule PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-674190/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Page 14; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCAGTGTACATGGGCGCACGGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCGCACGGGGCA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                              hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.4%;
                                                                                                              receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 154; DB 6;
Pred. No. 1.6e-37
                                                                                                           insulin regulator construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                         IGFBP-1;
insulin;
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CC The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to cincrease fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly euglycaemic conditions complication of these effects can maintain nearly euglycaemic conditions complication in this properties confinition of the long-term complications of diabeties. The properties confined in those provided by secreted insulin, e.g. cinhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence
    Matches 103;
                                          Query Match
                                                                             Sequence 321 BP; 77 A; 111 C; 84 G; 49 T; 0 U; 0 Other;
                                                                                                                  represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 14; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-674190/72.
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                          Local
                      Similarity
      Conservative
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                    24.3%;
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Score 103; DB 6;
Pred. No. le-21;
0; Mismatches
                                    DB 6; Length 321,
  <u>,,</u>
  Indels
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  Gaps
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                      111 CACGGGGCACTCCCGGTGGTTCCTGGACTCTGGCCCCCAGTGTA 153
                                                                      103
 43
                                                                                                          51
                                                                                          ACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCG
CACGGGGCACTCCCGGGTTCCTGGACTCTGGCCCCCAGTGTA
                                                                      ACATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCG
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RESULT 8
ABK63701
ID ABK6
XX ABK6
XX ABK6
XX ABK6
XX ABK6
XX Rat
XX Rat;
XX Rat;
XW Rat;
XW AIff
XX ABK6
XX AB
30-JUL-2001; 2001WO-US023872
                                                                                                                                                                                                                                                                                                    WO200210453-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat; ss; hepatotoxin;
differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat sequence differentially expressed in response to a hepatotoxin #1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK63701;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag; EST; drug screening; on; centrilobular necrosis; steatosis.
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                                                                                                                                                                                                                                                                                                                                                RESULT 9
                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                         CC expression in a tissue or cell sample exposed to the compound of two or compression in a tissue or cell sample exposed to the compound of two or come genes listed in the specification, where differential expression of come the genes is indicative of at least one toxic effect or progression. The compounded can also be used to identify an agent which modulates the toxic cell. The methods utilise a set of at least two probes (on a solid compound modulates in a compounded compounded in the specification, a computer compound in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, a computer compounded in the specification, a computer compounded in the specification, a computer compound a user interface to view the information used to present information compounded in the specification in the specification compounded is useful for elucidating global changes in gene expression level in a tissue or cell of at least one gene containing and toxicity markers in considering toxicity markers in a compound or agent. He genes and considering the expression and for identifying toxicity markers for the considering or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is constructed in a perpension and compound or agent. Hepatotoxicity is generated in a perpension and compound or agent. Hepatotoxicity is constructed in the specification of the physiological state of tissue or cell exposed to a compound or agent. Hepatotoxicity is constructed in the specification of the physiological state of the second of the construction and constructed in the specification of the construction of the physiological state of the second of the second of the specification of the physiological state of the second o
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02-NOV-2000;
11-MAY-2001;
15-MAY-2001;
22-MAY-2001;
06-JUN-2001;
                                                                                                                                                                                                                                                                                                                                             Sequence 1500 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells. Also included are methods of predicting at least one toxic effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     global changes in gene expression in tissues or cells exposed to toxin and comparing these to gene expression in unexposed tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       compounds or the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-2001;
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                                                                                                                                                                                                                                                                           Local
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                                                                                            CACTTCCGCTACTAGCTA 418
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                                                                                                                                                                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1608; 239pp; English
                                                                    CACTTCCGCTACTATCTA 85
                                                                                                                                                            CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                          differentially
                                                                                                                                                                                                                                                                                                                                                                                                                is an expressed sequence tag (EST) or cDNA derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ); 2000US-0222040P.
); 2000US-0244880P.
); 2001US-0290029P.
); 2001US-0290645P.
); 2001US-0292336P.
); 2001US-0297457P.
); 2001US-0297457P.
); 2001US-0298844P.
); 2001US-0303459P.
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOGIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                relates to methods for predicting toxic effects of the progression of these toxic effects by determining
                                                                                                                                                                                                                                                                                                                                           336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INC
                                                                                                                                                                                                                                                                      18.1%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                        expressed
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                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                         Score 76.4; DB 6; Pred. No. 3.1e-13;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      in response to a hepatotoxic
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                                                                                                                                                                                                                                                                                            Length 1500;
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                                                                                                                                                                                                                                                                                                                                                                                                             from a gene
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IJ ADB58201

ADB58201 standard; DNA; 1500 BP

RESULT 10 ADB52710

ADB52710 standard; DNA; 1500

ВP

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                                                                                                                                                                                   The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile conference of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where conferential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hapatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in cellver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                      Matches
                                                                                                                                   Query Match
Best Local
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15-MAR-2002;
15-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3227; 1156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-689530/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2003; 2003WO-US003194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003064624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxic; toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxicity-related gene, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB58201;
                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening;
                                                                                   341 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC 400
83
                                                                                                                      77;
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                                                                                                                                    Similarity
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                   CACTTCCGCTACTAGCTA 418
                                                                                                                                                                                   1500
                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOGIC INC.
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2002US-0364055P.
2002US-0436643P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                 BP; 336 A; 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxicity assay;
                                                                                                                                   18.1%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IJ
85
                                                                                                                   Score 76.4; I Pred. No. 3.1e 0; Mismatches
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                                                                                                                                                                                   380 G;
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                                                                                                                                                                                   376 T;
                                                                                                                                      .1e-13
                                                                                                                                                   DB 10;
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                                                                                                                                                                                   0 U;
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                                                                                                                      Indels
                                                                                                                                                   Length 1500;
                                                                                                                                                                                   0 Other;
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                                                                                                                      0,
                                                                                                                      Gaps
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11-APR-2002;
19-APR-2002;
19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                   04-FEB-2002;
13-MAR-2002;
08-APR-2002;
10-APR-2002;
                                                                                                                                                                                                                                   10-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening;
                                                                                                                                                                                                                                                                                                                                                       04-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primary rat hepatocyte toxicity modelling related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2003
                                                                                                                                                                                                                                                     10-APR-2002;
(GENE-) GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rat
                                                                                                            2002US-0363534P

2002US-0370248P

2002US-0371134P

2002US-0371135P

2002US-0371150P

2002US-0371413P

2002US-0373601P

2002US-0373601P

2002US-0373602P

2002US-0373602P

2002US-0378652P

2002US-0378652P

2002US-0378653P
                             2002US-0378665P.
2002US-0394230P.
2002US-0394253P.
2002US-0407688P.
2003US-0442900P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatocyte toxicity modelling; gene; ds
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COGIC
                                                                                                                                                                                                                                                                                                                                                       2003WO-US003482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:3252.
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Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox 2003-731472/69.

for

Mendrick Elashoff

χ, Ζ,

Porter

Z,

Johnson

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Higgs

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Castle

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Claim 44; SEQ ID NO 3252; 874pp; English

the compound, and comparing the gene expression profile to a universe the compound, and comparing the gene expression profile to a universe comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database toxicity modelling related gene sequence from the

Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;

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Query Match
Best Local Similarity
Matches 77; Conserv
Conservative
       18.1%;
98.7%;
0
Score 76.4; Di
Pred. No. 3.1e
0; Mismatches
        .1e-13;
                  DB
                  10;
Indels
                  Length
                  1500;
٥,
Gaps
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0;

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RESULT 11
ABT41911
XX ABT41
XX ABT41
XX ABT41
XX ABT41
XX Toxic
XX Toxic
XX Toxic
XX Toxic
XX Toxic
XX Attl
AN Attl
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21-FEB-2002;
15-MAR-2002;
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01-NOV-2001;
21-NOV-2001;
06-DEC-2001;
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10-JUL-2001;
28-AUG-2001;
27-SEP-2001;
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13-JUN-2001;
19-JUN-2001;
10-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-2002
08-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-2001;
21-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxic effect; gene expression profile; renal toxicity; toxicity marker;
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2002US-0370206P.
2002US-0370247P.
2002US-0372794P.
2002US-0371679P.
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2002US-0357842P.
2002US-0357843P.
2002US-0357844P.
2002US-0364134P.
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2001US-0330867P.
2001US-0331805P.
2001US-0336144P.
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2001US-0298925P
2001US-0303807P
2001US-0303808P
2001US-0303808P
2001US-0301804P
2001US-0315047P
2001US-0324928P
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'n Porter M, Johnson 7 Higgs B, Castle P Elashoff M;

WPI; 2003-148464/14.

Predicting at least one toxic effect of a compound, useful f modeling, comprises preparing a gene expression profile of a cell sample exposed to the compound, and comparing the gene profile to a database. e expression

Example 4; Page; 446pp; English.

The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues

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ID P72689
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XX Renal
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Matches 77
The invention relates to a method of predicting (the progression of) a toxic effect of a compound by preparing a gene expression profile of a kidney tissue or cell sample exposed to the compound and comparing the gene expression profile to a database, or detecting the level of gene(s) expression in a tissue or cell sample exposed to the compound, where differential gene expression compared to a control indicates a toxic effect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are useful as toxicity markers in drug screening and toxicity assays. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; toxic effect; gene expression profile; kidney tissue; differential gene expression, toxicity progression, toxicity marker; drug screening; toxicity assay; kidney pathology; nephritis; kidney necrosis; glomerular injury; tubular injury; focal segmental glomerulosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease physiological states, or disease progression. This polymucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this pate did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
                                                                                                                                                                                                  Claim 11;
                                                                                                                                                                                                                                                    Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-2003; 2003WO-US037556
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98.7%;
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No. 3
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Matches
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                                                                                                                                                                           methods are useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis, kidney necrosis, glomerular and tubular injury, or focal segmental glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent. The kit is useful for predicting or modelling the toxic response of a test compound, for monitoring the progression of renal disease states, for identifying genes that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the method of the invention. (Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic forms part of the princed specification, but was obtained in electronic forms the control of the princed specification.
                                                                                                          Sequence 1500 BP; 336 A; 408 C; 380 G; 376 T; 0 U; 0 Other;
                                                                                                                                                          format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
1 Similarity 77; Conserv
  Conservative
                         18.1%;
98.7%;
  0;
Score 76.4; DB 12
Pred. No. 3.1e-13;
); Mismatches 1
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401 CACTTCCGCTACTAGCTA 68 æ CACTTCCGCTACTATCTA CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC 85 418 67

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22-AUG-2001 AAH22429; AAH22429 standard; (first entry) DNA; 5001 ₿₽

Identification; toxic; hepatotoxic; differential insulin-like growth factor binding protein nucleotide sequence gene expression; NSAID;

Rattus norvegicus.

non-steroidal antiinflammatory

drug;

gg

31-MAY-2001.

21-NOV-2000; 2000WO-US032049

22-NOV-1999; 18-FEB-2000; 20-NOV-2000; 2000US-0183531P. 2000US-00717321. 99US-0166923P.

(CURA-) CURAGEN CORP

Gould-Rothberg BE, Dipippo VA, Ramseh TM, Gerwein **χ**

Screening hepatotoxic expressing RISKMARKER with reference populat population agent comprises contacting test cell population or INJURYMARKER with agent, comparing expression tion and identifying difference in expression comparing expression

Disclosure; Page 22-24; 76pp; English

ARESULT 13
AAH22429
ID AAH22
XX AAH22
AC AAH22
XX Ident
XX Ident
KW Inon-s
XX WO200
XX WO200
XX WO200
XX WO200
XX WO21-N0
XX PD 31-N0
PR 20-N0
PR 20-N0
PR 18-FE
PR 20-N0
XX CURA
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X The present invention describes a method of screening a test agent for hepatotoxicity. The method comprises: (a) providing a test cell population comprising a cell capable of expressing one or more nucleic acid sequences selected from the group consisting of RISKMARKER 1-8 and the test cell population with a test

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RESULT 14
ABN95896
ID ABN95
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                      The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing and detecting the progression carcinoma or metastatic liver tumor in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease si disease progression; drug toxicity; drug efficacy; drug metabolism
                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2394; 298pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2000; 2000US-0237054P
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                                                                                                                                                                                                                                                                                                                                                                                                                                     level
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98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peres-Da-Silva
   to monitor disease states,
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Pred. No. 4.8e-13;
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                        WO200290580-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
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Pred. No. 3.
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Best Local Similarity
Matches 141; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to detecting the presence or diagnosing the risk of a liver cancer in a patient. The method involves detecting in a biological sample obtained from the patient aberrant expression of a gene encoding an insulin-like growth factor binding protein (1GPBP). The method is useful for detecting the presence or diagnosing the risk of a liver cancer or for screening agents in a patient. The agent is useful for the manufacture of a medicament for treating and/or preventing liver cancer. The present sequence represents a human IGPBP-1 polypeptide encoding genomic DNA (GenBank Accession No. M74587)
                                                                                                                                                                                                                                                                                                                                                                        Sequence 6128 BP; 1504 A; 1497 C; 1504 G; 1623 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting the presence or diagnosing the risk of a liver cancer in patient comprises detecting aberrant expression of a gene encoding insulin-like growth factor binding protein.
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ilarity 66.5%;
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Result
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Listing first 45 summaries
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Match Length DB
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Copyright (c) 1993 - 2005
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XX05684 Rat L-PK ge
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AC097039 Rattus no
218922 H.sapiens D
U47654 Homo sapiens D
U47654 Homo sapien
AY316591 Homo sapien
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AC147942 Carollia
AC147942 Carollia
AC147944 Attelerix
AC148066 Canis fam
AC148066 Canis fam
AC148066 Bos tauru
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Bos tauru
Macropus
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ALIGNMENTS

RESULT 2 AR175909 LOCUS DEFINITION ACCESSION VERSION KEYWORDS AS7715 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL SOURCE ORGANISM 밁 Ś ORIGIN FEATURES COMMENT Matches Query Match Best Local : Bource y Match 100.0%; Score 51; DB 6; 1 Local Similarity 100.0%; Pred. No. 2.7e-06; hes 51; Conservative 0; Mismatches 0; 11 unidentified unidentified unclassified. Unknown. Unknown. 194 bp Sequence 1 from Patent WO9632489. A57715 A57715.1 GI:3713539 AR175909 194 bp Sequence 1 from patent US 6309878. AR175909 Other publication AU 5652396 961030 Other publication FR 2732978 961018. Location/Qualifiers Chen, R., Doiron, B. and Kahn, A. GLUCOSE. INDUCIBLE RECOMBINANT VIRAL PATENT: WO 9632489-A 1 17-OCT-1996; INST NAT SANTE RECH MED (FR) AR175909.1 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644" GI:17917208 DNA DNA VECTOR Length 194; Indels linear linear PAT 17-DEC-2001 PAT 03-MAR-1998 0; Gaps 0

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RESULT 3
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LOCUS
DEFINITION
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KEYWORDS
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ORGANISM
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Best Local :
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1 (bases 1 to 194)

S Chen, R., Doiron, B. and Kahn, A.
Glucose-inducible recombinant viral vector
AL Patent: US 6309878-A 1 30-0CT-2001;
Location/Qualifiers

194
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OS Rattus norvegicus (rat)
PN JP 1997313059-A/14
PD 09-DEC-1997
PF 31-JAN-1997 JP 1997018966
PF 31-JAN-1997 JP 199701896
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E14395
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E14395.1 GI:5709078
JP 1997313059-A/14.
Rattus norvegicus (Norway rat)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                        3194. .3218
                                                                                                                                                                                                       exon
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                                                                           exon
                                                                                                           intron
                                                                                                                                          exon
                                                                                                                                                                       intron
                                                                                                                                                                                                                                        intron
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                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                        /number=1 3219. .37
                                           /number=4
6284. .641
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                                                                           6152.
                                                                                                           6009
                                                                                                                                                                       3949
               6418
                          number=4
                                                                                                                                                                                                        3766.
                                                                                                                                                                                                                                                                                     organism='Rattus norvegicus'
                                                                                          'number=3
                                                                                                                          'number=3
                                                                                                                                                                                        number=2
                                                                                                                                                        number=2
                                                                                                                                                                                                                      number=1
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kinase.
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Pred. No. 2.
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                                                                                                                                                                       .5916
                                           .6417
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2.7e-06;
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; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 28-JUL-1999
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                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                     SOURCE
ORGANISM
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ACCESSION
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KEYWORDS
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AX827302
           ORIGIN
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                                                                                          FEATURES
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Best Local Similarity
                                                                                                                        JOURNAL
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                                                                         source
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                                                                                                      Boess, F., Suter-Dick, L. and Wolf, D. Methods for the toxicity prediction of a compound Patent: EP 1344834-A 36 17-SEP-2003; F. HOFFMANN-LA ROCHE AG (CH)
                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                 13011 bp
Sequence 36 from Patent EP1344834.
AX827302
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3'UTR
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative
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7665. .7817,7911. .8077,
9298. .9479,10163.
/product='Pyruvate
Location/Qualifiers
                       /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                         .13011
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/number=7
7665.
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/number=5
6921. .7191
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7453. .766
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7818. .791
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9480. .101
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8078. .9297
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Pred. No. 1.3e-06;
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number=10
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intron 32193765 /number=1 exon 37663948 /number=2 intron 39495916	/codon_start=1 /codon_start=1 /protein_id="CAA29169.1" /db_xref="GAA29169.1" /db_xref="G	TATA_Bignal 31683173 precursor_RNA 319411594 /note="primary transcript" exon 31943218 /number=1 /number=1 /number=1 CDS 5418664,69217191,73027452,76657817,79118077, 92989479.1016310269)	.1422 "direct repeat .1434 "direct repeat .3149 "put.CCAAT box	_region :	1 (bases 1 Cognet,M., L Structure of J. Mol. Biol 88011310 3309348	RESULT 5 RNLPKG RNLPKG RNLPKG RNLPKG RAT L-PK SEPINITION Rat L-PK SEPINITION RAT L-PK SEPINITION ROBER ROBE	Query Match 100.0%; Score 51; DB 6; Length 13011; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CATGGGCGCACTGCGGTGGTTCCTGGACTCTGGCCCCAGTGTA 51
repeat_region repeat_region ORIGIN	repeat_region exon repeat_region repeat_region repeat_region repeat_region polyA_site repeat_region repeat_region		intron exon intron	exon intron exon intron exon	exon intron exon intron	1 1 1 1	repeat_region repeat_region repeat_region repeat_region
7 7	0 · 11 · · 11 · 0 · 10 · 10 · 11 · 11	/number=9 92989479 /number=10 948010162 /number=10 95809588 /note=direct repeat 5" 9596 9809		/ number=5 69217191 / number=6 71927301 / number=6 73027452 / number=7 74537664 / number=7 76657817	. 4. 4. 4. 4.	="direct repeat 4" 5011 ="repetitive sequence 3 5027 ="direct repeat 4" 5500 ="tepetitive sequence 4 6008 er=3 er=3 6147	/number=2 40664071 /note="direct repeat 3" 40724387 /note="repetitive sequence 2" 43884393 /note="direct repeat 3" 45864542

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COMMENT
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AUTHORS
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SEGMENT
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      DEFINITION
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                                               RESULT 7
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Best Local
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Best Local
                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PK mRNA and introns (alt.)" prim_transcript 930. .>2717
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                                                                                                                                                                                                                                                                                                       intron
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                                                                                                                                                     45;
AC097039 231241 bp
Rattus norvegicus clone CH230-61E1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Draft entry
T.Noguchi, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Original source text: Rat DNA (library of J.Bonner), clone lambda-LPK30, and reticulocyte, cDNA to mRNA, clones pRPK[1,3]. Draft entry and printed copy of sequence for [1] kindly provided by T.Noguchi, 09-SEP-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noguchi,T., Yamada,K., Inoue,H., Matsuda,T. and Tanaka
The L- and R-type isozymes of rat pyruvate kinase are
a single gene by use of different promoters
J. Biol. Chem. 262 (29), 14366-14371 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pyruvate kinase.
1 of 4
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M17088.1 GI:
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Mammalia; Eutheria;
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M17088 J03455
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                                                                                                                                                                    Similarity
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                                                                                                                                                      Conservative
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                                                                                                                                                                                                             2191. .>2717
/note="PK intron B"
upstream of PstI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol type="genomic DNA"
/db xref="taxon:10116"
925. .>2717
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="PK mRNA and introns (alt.)"
934. >2717
                                                                                                                                                                                                                                                                            2008
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                                                                                                                                                                                                                                                                                                                             /note="L-pyruvate kinase"
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                                                                                                                                                                                                                                                            'number=2
                                                                                                                                                                                                                                                                                         note="PK intron A (alt.)"
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                                                                                                                                                                                                                                                                                                                                                               /note="PK intron A"
                                                                                                                                                                                                                                                                                                                                                                                 /note="R-pyruvate kinase"
|080. .2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           note="PK mRNA and introns
                                                                                                                                                  84.7%; Score 43.2; DB 10
93.8%; Pred. No. 0.00059;
ative 0; Mismatches 3
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DNA linear HTG 10-MAY-2003
*** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                 DB 10;
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                                                                                                                                                                               Length 2717;
                                                                                                                                                     Indels
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Allen, C., Allen, M., Albrocks, S., Amin, A., Angpilano, D., Allen, V., Allen, V., Albrocks, S., Amin, A., Angpilano, D., Anyalebechi, V., Aoyadi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyadi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barristead, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brom, M., Brom, M., Blay, C., Brich, D., Barber, M., Barristead, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brom, M., Bryant, N., Buhay, C., Brich, P., Burrell, K., Calderon, E., Chan, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen
Submitted (10-MAY 2003) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:24819342.
                                                                                                                                                                                                                                                                      Submitted (06-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
Direct Submission
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                                                                                                                                                                                               Rat Genome Sequencing Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                      GGGCGCACGGGGCACTCCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 231241: contig of 231241 bp in length.
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Center clone name: CH230-61E1

Center clone name: CH230-61E1

Center clone name: CH230-61E1

Center clone name: CH230-61E1

Assembly program: Atlas 3.0;

Consensus quality: 210827 bases at least Q40

Consensus quality: 21095 bases at least Q30

Consensus quality: 216056 bases at least Q20

Consensus quality: 216056 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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clone_end:T7"
68569_.69982
/note="wgs_end_extension
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755. .1528
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clone_end:Sp6
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-61E1"
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93.8%;
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Pred. No. 0
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1 (bases 1 to 8409)

Lenzner; C., Nurnberg, P., Jacobasch, G. and Thiele, B.J.

Complete genomic sequence of the human PK-L/R-gene includes four intragenic polymorphisms defining different haplotype backgrounds of normal and mutant PK-genes DNA Seq. 8 (1-2), 45-53 (1997)

98182587
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8409 bp DNA linear PRI 05-AUG-1999
Homo sapiens pyruvate kinase PK-R isoenzyme gene, partial cds; and
pyruvate kinase PK-L isoenzyme gene, complete cds.
U47654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                            Submitted (30-JAN-1996) Peter Nuernberg, Institute for Medical Genetics, Charite Medical School of the Humboldt-University Be Schumannstr. 20/21, Berlin 10098, Germany
                                                                                                                                               2 (bases 1 to 8409)
Lenzner,C., Nuernberg,P., Jacobasch,G. and Thiele,H.-J.
Direct Submission
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Submitted (03-DEC-1992) de Medicis
Biochimie, 12e avenue Nord, Fleurin
                                                                           Schumannstr. 20/21, Berlin 10098, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Unpublished
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/db xref="taxon:9606"
/cell_type="fanh-
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:1230588
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/citation=[1]
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90.7%;
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region of human liver pyruvate kinase
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Pred. No. 0.12;
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                 Rieder, M.J., Livingston, R.J., Daniels, M.R., Montoya, M.A., Chung, M.-W., Miyamoto, K.E., Nguyen, C.P., Nguyen, D.A., Poel, C.L., Chung, M.-W., Miyamoto, K.E., Nguyen, C.P., Nguyen, D.A., Poel, C.L., Robertson, P.D., Schackwitz, W.S., Sherwood, J.K., Witrak, L.A. and
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 13322)
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Homo sapiens pyruvate kinase, liver and RBC (PKLR)
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TAFFQQQQLPAAMADTFLEHLCLLDIDSEPVAARSTSIIATIGPASRSVERLKEMIKA
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GGPESEVELVKGSQVLJVTVDPAFRTRGWANTVMVDYPMIVRVPVGGRIYIDDGLISL
VQKIGPEGLVTQVENGGVLGSRKGVNLPGAQVDLPGLSEQDVRDLRFGVEHGVDIVF
AS FVRKASDVAAVRAALGPEGHGIKISKIENHEGVKRFDEILEVSDGJMAVALDGAG
SFVRKASDVAAVRAALGPEGHGIKISKIVALPGAGVEHERDTEVSDGJMAVALDGAG
EIPAEKVFLAQKOMMIGKCNLAGKPVVCATQMLESMITKRPFTRAETSDVANVALDGAG
CIMLSGETAKGNPPVEAVKMQHAIAREABAAVHRQLFEELRRAAPLSRDPTEVTAIG
AVEAARKCCAAAIIVLTTTGRAQLLSRYRPBAAVLAVTRSAQAARQVHLCRGVFPLL
READARKCCAAAIIVLTTGRAQLLSRYRPBAAVLAVTRSAQAARQVHLCRGVFPLL
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join(478. .553,1145. .1327,2508. .2599,2696. .2827,2961. .31
3510. .3780,3877. .4027,4672. .4824,4919. .5085,6325. .6506,
7572. .7678)
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yrpvalaldtkopelirgiloggpesevelvsksgslylutvdpaptrtronamymvdyp
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kprptraetsbvanavldgadcimlscstrylagkomigrchlagkpvcatqmleshavyhrqli
peelrraaplsrdptevtaigaveaafkccaaaiivltttgrsaqllsryppraavia
vtrsaqaarqyhlcrgypplatreppeaimaddvdrrvQfgiesgklrgflrvgdlvi
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2961. .3147,3510. .3780,3877. .4027,4672. .4824,4919.
6325. .6506,7572. .7678)
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3510. .3780,3877. .4027,4672. .4824,4919. .5085,6325. .6506,
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/db_xref="GI:1230590"
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3510. .3780,3877. .4027,4672. .4824,4919. .5085,6325. .6506,
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Pred. No. 0.068;
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Submitted (06-JUN-2003) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: http://egp.gs.washington.edu).
Location/Qualifiers
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EHGUDIVFASEVRKASDVAAVRAALGPEGHGIKIISKIENHEGVKRPDEILEWSDGIN
VARGDLGIEIPAEKVFLAQKOMNIGRCNLAGKPVVCATQMLESMITKPRPTRAETSDVA
                         /replace="c"
2081. .4840
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/rpt_family="MIR"
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PTEVTAIGAVEAAFKCCAAAIIVLTTTGRSAQLLSRYRPRAAVIAVTRSAQAARQVHL
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'gene="PKLR"
                                                                                                                                                                                                                                                                                                                                                  frequency="0.02"
replace="a"
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join(550. .649,1665. .1847,6189. .6280,6377. .6508,6643. .6829
17193. .7463,7560. .7710,8355. .8507,8602. .8768,10008. .10189,
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5643. .6829,7193. .7463,7560. .7710,8355. .8507,8602. .8768,
,0008. .10189,11267. .11691)
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frequency="0.42"
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2457._.2758
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frequency="0.03"
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                                                                                                                                                                                                                                                                                                                                                                   867
                                                     Submitted (13-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 14, 2003 this sequence version replaced gi:30523877.
                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133525)
Glithero,R.
                                                                                                                                                                                                                                                     sequence.
AL713999
                          Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                              AL713999 133525 bp DNA linear PRI Human DNA sequence from clone RPI1-263K19 on chromosome
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                           Direct Submission
                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                      AL713999.28
                                                                                                                                                                                                                                                                                                                                                                CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                      71.8%;
nilarity 90.7%;
Conservative
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7566
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'frequency="0.01"
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replace="t"
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frequency="0.01"
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frequency="0.01"
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frequency="0.01"
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                                                                                                                                                                                                                                        GI:30722340
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.6; DB
Pred. No. 0.063;
0; Mismatches
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9; 4

Length 13322; Indels

0

Gaps

0

13-MAY-2003 1, complete

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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129358 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 129316
                                                    Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,
Boulfard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B.,
Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P.,
Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Margulies, D., Paguirigan, C., Portnoy, M.E., Prasad, A., Puri, O.,
Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C.
Stantripop, S., Thomas, J. W., Thomas, P.J., Tsipouri, V., Vogt, J.L.
Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RP11-263X19 is from the library RPCI-11.1 constructed by the group of pierer de Jong For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC148047
AC148047.2 GI:45544599
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions were either double-stranded or sequenced with an aliternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur 1 (bases 1 to 192549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otolemur garnettii (small-eared galago)
Otolemur garnettii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC148047
Otolemur garnettii clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ordered
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                           Comparative Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-263K19"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .. .133525
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Pred. No. 0.041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192549 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH256-360P11, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                               Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 133525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE,
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclomes, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a process of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717
Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717
Sequencing Center, 8717
Sequencing Center, 8717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-JAN-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 192549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green, E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Mar 18, 2004 this sequence version replaced gi:41386816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 38219: contig of 38219 bp in length
38220 38319: gap of unknown length
38320 77219: contig of 38900 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                    114116
114216
126275
126375
152698
152798
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38320
77220
77320
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Consensus quality: 190022 bases at least Q40
Consensus quality: 191157 bases at least Q30
Consensus quality: 191179 bases at least Q20
Insert size: 149000; agarose-fp
Insert size: 191949; sum-of-contigs
Quality coverage: 11.55x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 360P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: nisc_zoo@nhgri.nih.go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: NISC
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/mol_type="genomic DNA
/db_xref="taxon:30611"
/clone="CH256-360P11"
                                                                                                                           organism="Otolemur garnettii"
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- Genome Center
                                                                                                                                                                                                                                                  167006:
192549:
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                                                                                  _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                        gap of contig
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contrig of 36796 bp in length
gap of unknown length
contrig of 12059 bp in length
                                                                                                                                                                                                                                              gap of unknown contig of 25543
                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown length contig of 26323 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                            Submitted (22-JAN-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 95718)
                                                            Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
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HTG; HTGS_PHASE2; HTGS_DRAFT.
Carollia perspicillata (Seba's short-tailed bat)
Carollia perspicillata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carollia perspicillata clone ordered minno
                                     On Mar 18, 2004 this sequence version replaced gi:41058168.
                                                                                                                            Green, E.D.
                                                                                                                                                                                                                                   Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae; Carollinae; Carollia.

1 (bases 1 to 95718)
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Center: NIH Intramural Sequencing Center
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AC148125 clone CH256-404N19 (center project name fx:
38320. .77219
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167007. .192549
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152798. .166906
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1. .30749
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126375. .152697
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114216. .126274
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47203,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * This sequence will be replaced

* the accession number will be preserved.

* the accession number will be preserved.

1 18008: contig of 18008 bp in length

* 18009 18908: gap of unknown length

* 22120 2219: gap of unknown length

* 22120 2219: gap of unknown length

* 31750: contig of 9531 bp in length

* 31750: sontig of 9531 bp in length

* 31851 53063: contig of 21213 bp in length

* 53064 53163: gap of unknown length

* 53064 53163: gap of unknown length

* 53064 53163: contig of 42555 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 94695 bases at least Q40 consensus quality: 95070 bases at least Q30 Consensus quality: 95243 bases at least Q20 Insert size: 95100; agarose-fp Insert size: 95100; agarose-fp Quality coverage: 11.88x in Q20 bases; sum-of-contigs Quality coverage: 11.15x in Q20 bases; sum-of-contigs
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Center clone name: 472003
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                                                                                                                                                                                                                                                                                                                /note="assembly_fragment
clone_end:SP6
vector_side:left"
53164. .95718
                                                                     31851.
                                                                                                                             /note="assembly_fragment"
22220. .31750
                                                                                                                                                                                            18909.
                                                                                                                                                                                                                   /note="clone overlaps with GenBank Accession Number AC148052 clone 593F8 (center project name gda)"
                       /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="The Green Lab"
/note="egreen@nhgri.nih.gov"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA
/db_xref="taxon:40233"
/clone="47203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Carollia perspicillata"
/mol_type="genomic DNA"
                                                                                         note="assembly_fragment"
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/note="assembly_fragment
clone_end:T7

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                                                                                                                              The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least & average.
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                                         coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associawith a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-MAR-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Mar 18, 2004 this sequence version replaced gi:41058180.
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HTG; HTGS PHASE2; HTGS DRAFT.
Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green, E.D.
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Atelerix albiventris clone LB4-218C14, WORKING DRAFT SEQUENCE, 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGTCACGGGACACTCCCGTGGTTCTTGGACTCTGACCCCTGGT 24252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 136883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 136883)
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                                                                                                                                                                                                                                                                                                                                                    Center project Information
Center project name: dut
Center clone name: 218C14
                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
Sequencing vector: plasmid; n/a; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: NIH Intramural Sequencing Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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    Summary Statistics

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Pred. No. 1
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                                                                    base is associated
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106362
106462
125086
125186
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86150
96129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_end:SP6
                                         clone_end:T7
                                                                                                                                                                                      96229. .106361
                                                                                                                                                                                                                                  86150. .96128
                                                                                                                                                                                                                                                                                                                                                         54372. .86049
                                                                                                                                                                                                                                                                                                                                                                                                  37524. .54271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector
                                                            note="assembly_fragment"
                                                                                            125186. .136883
                                                                                                        /note="assembly_fragment"
                                                                                                                                                                                                     note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment
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                                                                                                                                                         note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                    note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                     'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .12022
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* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* T474 7573: contig of 7473 bp in length

* 7574 12022: contig of 4449 bp in length

* 12023 12122: gap of unknown length

* 12123 37423: contig of 25301 bp in length

* 37524 54271: contig of 16748 bp in length

* 37524 54271: contig of 16748 bp in length

* 54372 86049: contig of 31678 bp in length

* 54372 86049: contig of 31678 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 135309 bases at least Q40
Consensus quality: 135732 bases at least Q30
Consensus quality: 135732 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 136083; sum-of-contigs
Quality coverage: 12.45x in Q20 bases; sum-of-contigs
61666. .136883
/note="clone overlaps with GenBank Accession Number AC148054 clone LB4-124B14 (center project name dus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Atelerix albiventris"
/mol_type="genomic DNA"
/db_xref="taxon:9368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="clone overlaps with GenBank Accession Number
AC148055 clone LB4-416H21 (center project name duv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="LB4-218C14"
/clone_lib="LB4"
/note="BAC resource: http://bacpac.chori.org/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86149: gap of unknown length
96128: contig of 9979 bp in length
96228: gap of unknown length
106361: contig of 10133 bp in length
106461: gap of unknown length
125085: contig of 18624 bp in length
125185: gap of unknown length
136883: contig of 11698 bp in length.
   (center project name dus)"
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AC148054/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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Best Local Similarity
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                                                                                                                    The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Daki, N., Engle, J., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B.,
Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Laric, P.,
Larson, S., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Margulies, E.H., Masiello, C., Portnoy, M.E., Prasad, A., Puri, O.,
Margulies, N., Schandler, K., Schueler, M.G., Shah, K., Sison, C.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L.,
Wetherby, K.D., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-APR-2004) NIH Intramural Sequencing Center, Grovement Circle, Gaithersburg, MD 20877, USA On Apr 7, 2004 this sequence version replaced gi:41386823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC148054.2 GI:46250790
HTG; HTGS_PHASE2; HTGS_DRAFT.
Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC148054 153222 bp DNA linear HTG 07-APR-
Atelerix albiventris clone LB4-124B14, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-JAN-2004) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ordered pieces.
                                                                                                         with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comparative Sequencing Initiative
                     Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: dus
Center clone name: 124B14
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submission
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81.4%;
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Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멂
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by the finished sequence as soon as it is available and the accession number will be preserved.

1 888: contig of 888 bp in length 889 988: gap of unknown length 989 24329: contig of 23341 bp in length 24330 24429: gap of unknown length 24430 33974: contig of 9545 bp in length 33975 34074: gap of unknown length 34829: contig of 10755 bp in length 44830 44929: gap of unknown length 14830 44929: gap 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_end:T7
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                                                 /note="assembly_fragment"
106506. .139816
                                                                                                                                                                                                                          77992. .80425
                                                                                                                                                                                                                                            note="assembly_fragment"
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/clone_lib="LB4"
|note="BAC resource: http://bacpac.chori.org/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Atelerix albiventris"
'note="assembly_fragment'
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db_xref="taxon:9368"
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Search completed: September 1, 2005, 03:26:37 Job time: 327.549 secs
                                                                                                                                                                                                        ORIGIN
                                                                                                                                 Query Match 59.2%; Score 30.2; DB 2; Length 153222; Best Local Similarity 81.4%; Pred. No. 4.9; Matches 35; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                     misc_feature
                                                                139917. .148451
/notee=massembly_fragment=
148552. .153222
/notee=massembly_fragment
clone_end:SP6
vector_side:right=
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Title:
Perfect score:
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   Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
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                                                                                                                            8: 9 9 5 *
Query
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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47.5 47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.8	47.8	47.8
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CE123626 CE256374	-	CE075799	CE668350	CK627560	BM943713	CN670899	CE338459	BM944811	CN669363	CE699841	CE200317	CO739485	CB177707	CG481325	CE418242	BQ940337	CC972844	BF101581
tigr-gaa- tigr-gaa-	mk25e02.y	tiar-ass-	tigr-gas-	io05f01.y	UI-M-EHOP	A0898H12-	tigr-gss-	UI-M-EHOP	A0878H10-	tigr-gas-	tigr-gaa-	S1LB06a23	in94f04.x	OST13706	tigr-gss-	AGENCOURT	ZUACY29TH	601753396

ALIGNMENTS

	source	FEATURES												COMMENT	JOURNAL		TITLE				AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AZ840793	RESULT 1
/organisms mus musculus" /organisms mus musculus" /otoltypes"genomic DNA" /strain="C57BL/6J" /db_xref="texon:10090" /clone="UUGC2M0138D02" /sex="Male" /sex="Male" /sex="Mouse 10kb plasmid UUGC1M library" /clone lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Labbratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA	1	Location/Qualitiers	High quality sequence stop: 659.	Class: plasmid ends	Plate: 0138 row: D column: 02	:h: 10000	Email: ddunn@genetics.utah.edu	Fax: 801 585 7177	Tel: 801 585 5606	4	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	University of Utah	-	Contact: Robert B. Weiss	Unpublished (2000)	plasmid inserts	Mouse whole genome scaffolding with paired end reads from 10kb	Niederhausern, A. and Wright, D., Weiss, R.	Reilly.M. Rose.M. Rose.R. Stokes.R. Tingey.A. von	Islam.H. Longacre.S. Mahmoud.M. Meenen.E. Pedergen.T.	Dunn.D. Aovagi.A. Barber.M. Beacorn.T. Duval.B. Hamil.C.	1 to 659)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus		Mus musculus (house mouse)	GSS.	AZ840793.1 GI:13010701		clone UUGC2M0138D02 R, genomic survey sequence.	2R Mouse 10kb plasmid UUGC1M library Mus musculu	AZ840793 659 bp DNA linear GSS 20-FEB-2001		

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Query Match
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                              Plate: 135 row: G column: 20
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with
v0.980904.e. Vector identified by cross_match with the -mi
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527229 MARC 3BOV Bos ta
BM286990
BM286990.1 GI:17996016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11282978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARC 3BOV Bos taurus cDNA 5', mRNA sequence
/clone lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar
                                                                                              /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                         organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.3%;
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Pred. No.
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0.00051;
hes 0;
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REFERENCE AUTHORS

RESULT 2 BM286990

밁 Ś ORIGIN

Matches

DEFINITION ACCESSION

VERSION KEYWORDS

SOURCE

ORGANISM

PUBMED COMMENT

JOURNAL MEDLINE

TITLE

FEATURES

source

BE867308

907

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RESULT 4
BE867308
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BF105536/c
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                                                                                                                                                                                                                              4 GGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Ir
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 827)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM871 row: m column: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 28 High quality sequence stop: 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4045620"
/lab_host="DH10B (T1 phage-resistant)"
/clone=lib="NIH_MGC_75"
/clone=lib="NIH_MCC_75"
/clone=lib="NIH_MC_75"
/clone=lib="NIH_MCC_75"
/clone=lib="
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75.0%;
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Pred. No. 78;
0; Mismatches
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Pred. No. 2
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On Feb 13, 2001 this sequence version replaced gi:31066600. Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and Cloned
into the Not I and EcoR V sites of the pomVSPORT 6 vector: Library
was normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL528750 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo CDNA Clone CSODD001YN07 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 765)
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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AL528750.3 GI:45703809
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene
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BE867308.1 GI:10316084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MCC_65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
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/mol_type="mRNA"
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Canis familiaris
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                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CSODD001CG04NP1&c=6514.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kirkness EF
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                                                                                                                                                                                                                                                                                                         shotgun
                                                                                                                                                                                                                                                                                                                          ekirknes@tigr.org
                                                                                                                                           /clone lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared from
peripheral blood"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODD001YN07"
                                                                                                                                                                                                                organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
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                                                                                                                                                                                                 db_xref="taxon:9615"
                                                                      50.6%;
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Pred. No. 2.7e-
0; Mismatches
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Pred. No. 3e+0
0; Mismatches
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3e+02;
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CATGGGCACAGTGGGCACTCCCGGCCGTCCCTGGCCTC

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                                                        Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 739)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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 Geron Corporation 230 Constitution
                             Contact: Brandenberger R
Regenerative Medicine
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CN360924.1
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The Institute for Genomic
Department of Eukaryotic G
Rockville, MD 20850, USA
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Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
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tigr-gss-dog-17000319093723 I
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Fax: 301-838-0208
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/clone lib='Dog Library"
/note="Site_1: BstXI; Libraries were prepared peripheral blood"
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/strain="Standard Poodle"
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mol type="genomic DNA"
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Pred. No. 3.1e+0
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1 (bases 1 to 225)

Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

extension cloning of partial genes

Genomics 84 (1), 205-210 (2004)
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Contact: Fu GK
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Fax: 650 473 7760
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                                                                                                                                                GCACGTGGACCACCCGGGGAGCCTGGACTCTGGCATCCAG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells" /clone lib="GRN EB" /note="oligo dT primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."
                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA,"
/db_xref="taxon:9606"
/clone 11b="FLP"
/note="Vector: pDrive Cloning Vector"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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FLP Homo sapiens cDNA,
                  GI:40278321
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77.5%;
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Pred. No. 3.1e+02;
                                                                                                                                                                                                                              Score 25.6; DB 6; Pred. No. 3.4e+02;
                                                                                                                                                                                                               Mismatches
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cDNA,
                                               mRNA linear
mRNA sequence.
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5', mRNA Bequence.
BQ056161
BQ056161 GI:19815501
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1021)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L. Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 229)
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incyte Genomics,
                                                                                                                                                                                                                                                                                                                      nttp://image.llnl.gov
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                                                                                                                                                                                                                                                                               quality sequence
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/tissue_type="lymphoma, cell line"
/lab host="DH10B (phage resistant)"
/clone_libe"NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory
                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:5808449"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                             ty sequence stop: 669
Location/Qualifiers
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/note="Vector:
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77.5%;
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RESULT 12
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Best Local Similarity
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DG1_17_E
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CC453282 259 by ZMMBBC Zea mays genomic survey sequence. CC453282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 472)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: dark-grown seedlings
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                                                                                                                                                                                                                                                                                                                /clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site 1: XhOI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II
Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sorghum bicolor"
                                                                                                                                                                                                                                            49.48;
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Pred. No. 4.8e+
0; Mismatches
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Pred. No. 3.7e+02;
D; Mismatches 9;
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(DG1) Sorghum bicolor cDNA,
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                                     clone ZMMBBc0344B20
                                                                                                                                                                                                                                                             Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                        1 (bases 1 to 334)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           BI006710 334 bp mRNA linear RC5-RT0053-110101-011-H09 RT0053 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003b)
Ludwig Institute for Cancer Rese
Rua Prof. Antonio Prudente 109,
                                        Contact: Simpson A.J.G. Laboratory of Cancer Ge
                                                                                                                  Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                  sequence tags
                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                          Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Class: BAC ends
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The Plant Genome Initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 Frelinghuysen Road, Piscataway,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bharti, A.K.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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1 (bases 1 to 259)
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/note="Vector:
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ute for Cancer R
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                  Research
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4 andar,
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01509-010, Sao
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COMMENT
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ORGANISM
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CE744237/c
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VERSION
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                             14512627
Contact: Kirkness EF
The Institute for Genomic Research
The Institute for Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 403)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence CE744237
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tigr-qss-dog-17000369534847 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-RT0053-
110101-011-H09&t3=2001-01-11&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                      The dog genome: survey sequencing and comparative analysis considered 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Location/Qualifiers
                                                                                                                                                                                                                            Fax: 301-838-0208
                                                                                                                                                                                                                                               Tel: 301-838-0200
                                                                                                                                                                                                                                                                Department of Eukaryotic Rockville, MD 20850, USA
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                                                                                                                                                                                   shotgun
                                                                                                                                                                                                    ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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peripheral
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/note="Site_1: BstXI; Libraries were prepared from
                                                                                                                                                            ocation/Qualifiers
                                                                                                                   organism="Canis familiaris"
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Query Match

Score

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Gapop 10.0 , Gapext 1.0
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. is derived by analysis of the total score distribution.

Adn04235 Antipsori	ADN04235	12	3138	47.8	24.4	20	
Abn95218 Gene #171	ABN95218	6	3138	47.8	24.4	19	
Aaa62683 Human Zic	AAA62683	w	3138	47.8	24.4	18	
Adh74825 Human Not		12	55001	48.2	24.6	17	
Adg88848 Human Not		12	55001	48.2	24.6	16	
	ADE83614	12	26	51.0	26	15	
Ade83566 L-pyruvat	ADE83566	12	27	52.9	27	14	
Ade83567 L-pyruvat	ADE83567	12	27	52.9	27	c 13	
Ade83565 ChREBP pu	ADE83565	12	30	58.8	30	12	
Abx15380 Rat liver	ABX15380	თ	51	94.1	48	c 11	
Abx15379 Rat liver	ABX15379	g	48	94.1	48	10	
Adp72914 Renal tox		12	13011	100.0	51	9	
Abt42448 Toxicity	ABT42448	10	13011	100.0	51	8	
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Abx15376 Rat insul	ABX15376	σ	423	100.0	51	σ	
Abx15375 Rat insul	ABX15375	σ	372	100.0	51	o v	
Abx15374 Rat insul	ABX15374	9	321	100.0	51	0	
Abx15373 Rat insul	ABX15373	σ	270	100.0	51	w	
Aat43002 Rat type	AAT43002	N	194	100.0	51	N	
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	SUMMARIES						

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24	24	24	24	24									24	24	24	24	24	24		24				24.4
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AAK77581	AAS35064	AAS30237	AAS28996	ADF70603	AAH78712	AAI99548	ABT17029	ABZ42551	AAS98070	AAV38513	AAK77579	ACC84331	AA168793	ADO29943	ABZ42892	ABV73365	AAS98133	AAK77580	ACH79332	ACH93032	AAT43003	ADQ22099	ADR25048	AUQ1/359
Aak77581 Human imm	Aas35064 DNA #14	Aas30237 DNA encod	Aas28996 Genomic	Adf70603 Orphan re	Aah78712 Human EX3	Aai99548 Human exp	Abt17029 Human MP2	Abz42551 Human G	Aas98070 Human DNA	Aav38513 Human 7-t		Acc84331 Human hpl	Aai68793 Human MAR	Ado29943 Human GPO				Aak77580 Human imm	Ach79332 Human gen	Ach93032 Human gen	Aat43003 Rat type	Adq22099 Human sof	Adr25048 Breast ca	Addi/359 Human Bor

RESULT 1 ABX15371 IID ABX11 XX ABX11 XX ABX1 AC ABX1 AC ABX1 XX TO ABX1 AC A Rattus norvegicus. Rat glucose response element (GIRE) DNA. ABX15371; ABX15371 standard; DNA; 51 BP intracellular hormone 17-APR-2003 (first entry)

ALIGNMENTS

Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; catabolism; catabolism; catabolism; catabolism; catabolism; catabolism; catabolism; catabolism; betogenesis; ketoacidosis; hepatoma; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; receptor; insulin regulator construct; anabolic

US2002107198-A1.

08-AUG-2002

10-OCT-2001; 2001US-00972916

11-OCT-2000; 2000US-0239113P

(THUL/) THULE P M.

WPI; 2002-674190/72.

New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insuliver cells. ingulin in

Claim 7; Page 13; 37pp; English.

The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like gr growth

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RESULT 2
AAT14302
IID AAT14
XX AAT14
XX AAT14
XX AAT14
XX RAT
DT 16-J
DT 16-J
DT RAT
XX Gluc
KW Hypee
KW SS.
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Best Local S
Matches 51
                                                                                       Recombinant defective virus contg. heterologous gene under control of glucose inducible promoter - and infected mammalian cells, esp. for gu
                                                                                                                                                                                            WPI; 1996-477139/47.
                                                                                                                                                                                                                                                                                                                                                                               14-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-1996;
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                                                                                                                                                                                                                                                   'n
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                                                                 of,
                                                                                                                                                                                                                                                                                                              INST NAT SANTE & RECH MEDICALE
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                                                                 diabetes
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/label= L4 element
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40. .58
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/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                       Kahn
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s; gene therapy; viral vector;
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                                                                                       for gene
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Claim 4;

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glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growtl factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose response element; GRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new defective recombinant virus contains at least one heterologous gunder control of an expression signal inducible by glucose or its analogues. Preferably, the expression signal is derived from the 183 k region located 5' of the type L pyruvate kinase (L-PK) gene, especiall having the present sequence. Expression of the recombinant virus can k controlled by glucose levels, but insulin production can be stopped immediately by administering glucagon. This avoids the risk of hypoglycaemia caused by excessive insulin production. Mammalian cells infected by the virus can be implanted into liver, spleen, pancreas or intestine, to provide insulin secretion at predetermined sites. The virus full is provided insulin secretion at predetermined sites. The virus can be implanted into liver, spleen, pancreas or intestine, to provide insulin secretion at predetermined sites. The virus can be stopped to the virus can be implanted into liver, spleen, pancreas or intestine, to provide insulin secretion at predetermined sites. The virus can be stopped to the virus can be implanted into liver.
                                                                                   The invention relates to an insulin regulator construct comprising glucose response element (GIRE) of a liver pyruvate kinase (LPK) go
                                                                                                                                           Claim 9; Page 13-14; 37pp; English.
                                                                                                                                                                                                      New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insu
                                                                                                                                                                                                                                                                    WPI; 2002-674190/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intestine, to provide insulin section, in general diseases associated is useful in gene therapy to treat and/or prevent diseases associated with hyperglycaemia, particularly diabetes, but more generally can be with hyperglycaemia, particularly diabetes, but more generally can be
                                                                                                                                                                                                                                                                                                                                                      (THUL/) THULE
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic; intracellular hormone receptor; insulin regulator construct; anaboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insuliinsulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                                                                                                                                                                                                                                                                                                                                    New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
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                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                        9; Page 14; 37pp; English
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Pred. No.
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The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), to increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other

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RESULT 5
ABX15375/c
ID ABX153
XX ABX153
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XX Glucos
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KW fat cas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IG insulin-sensitive element; ISE; basal promoter; hyperglycaemia; ilinsulin-like growth factor binding protein-l; hypoglycaemia; glucotationsulin-like growth factor binding protein-l; hypoglycaemia; glucotaticoid; fat catabolism; protein catabolism; carbohydrate; glucocorticoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                          New insulin regulator cassette, useful e.g. for provides specific, glucose-inducible transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glucagon; euglycaemia; diabetes; fasting; ketogenesis; ketoacidosis; hepatocyte; hepatoma; cellular protein degradation; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX15375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat insulin regulator construct DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intracellular hormone receptor; insulin regulator construct; anabolic
                                                                                                                                                                                                                                                                                                                                 liver cells.
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ilarity 100.0%;
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Pred. No. 4.5
D; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                treating diabetes, expression of insulin
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RESULT 6
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      carbohydrates) and glucocorticoids and
                            to treat or prevent diabetic complications, to regulate insulin production, to modulate hyperglycaemia (without severe hypoglycaemia), increase fat catabolism and to retard protein catabolism. The construct provides stimulation of insulin expression by glucose (but not other
                                                                                                                                                The invention relates to an insulin regulator construct comprising a glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene promoter and an insulin-sensitive element (ISE) of an insulin-like growth factor binding protein-1 (GFBP-1) basal promoter. The construct is used
                                                                                                                                                                                                                                                                                                                 Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                     New insulin regulator cassette, useful e.g. for treating diabetes, provides specific, glucose-inducible transgenic expression of insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucose response element; GIRE; liver pyruvate kinase; LPK; ds; IGFBP-1; insulin-sensitive element; ISE; basal promoter; hyperglycaemia; insulin; insulin-like growth factor binding protein-1; hypoglycaemia; glucose; fat catabolism; protein catabolism; carbohydrate; glucocorticoid; rat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carbohydrates) and glucocorticoids and inhibition by glucagon so that a combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-differentiated hepatoma lines and insulin expression in these cells may have effects additional to those provided by secreted insulin, e.g. inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-674190/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thule PM;
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                                                                                                                                                                                                                                                                                                              Page 14; 37pp; English
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inhibition by glucagon so that a
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                                                                                                                                                                                                                                                                                                                                                                                                     storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT96631 standard; DNA; 13011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence represents a rat insulin regulator construct of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              combination of these effects can maintain nearly euglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, thus inhibiting the long-term complications of diabetes. The properties
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                                                                                                                                                                                                                                                                                                                                                                                                                                  rat cytosolic pyruvate kinase.
/number= 5
6921. .7191
/*tag= 1
                             6605. .6920
/*tag= k
                                               /*tag= j
/number= 5
                                                                                                                                                            /number= 3
6009. .6151
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/number= 2
5917. .6008
/*tag= f
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Matches 51
                                                                                This DNA encodes a Rattus norvegicus cytosolic pyruvate kinase. The storage lipid content of a seed is increased by reducing the activity endogenous cytosolic pyruvate kinase in the seed. This is applied to plants which accumulate storage procein and lipid in the embryo, particularly an oilseed plant such as soya, sunflower, sesame or especially rapeseed. Inhibitory enzymes involved in amino acid biosynthesis increases production of lipid by directing more of the precursor to the chloroplast
                                                                                                                                                                                                                                                                                                                                                         exon
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MITSUBISHI CHEM CORP
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              CATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
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                                Conservative
                                                                  BP;
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/number= 10
8078. .9297
/*tag=
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/*tag= u
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9298. .9479
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7302. .74
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28-AUG-2001;
27-SEP-2001;
27-SEP-2001;
01-NOV-2001;
21-NOV-2001;
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19-DEC-2001;
21-FEB-2002;
21-FEB-2002;
21-FEB-2002;
21-FEB-2002;
15-MAR-2002;
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10-JUL-2001;
10-JUL-2001;
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13-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxicity modelling related rat
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2001US-030380PP
2001US-030380PP
2001US-0303810P
2001US-03304928P
2001US-0330462P
2001US-0330462P
2001US-0331805P
2001US-0331805P
2001US-0331805P
2001US-035144P
2002US-0357843P
2002US-0357844P
2002US-0357844P
2002US-0357844P
2002US-035784P
2002US-0370144P
2002US-0370144P
2002US-0370144P
2002US-0370149P
2002US-037019PP
2002US-037019PP
2002US-037029PP
2002US-0372794PP
2002US-037279PP
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2001US-0297523P
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Mendrick D, Porter M, Johnson χ, Higgs В, Castle Ņ Elashoff M;

WPI; 2003-148464/14.

Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database.

Example 4; Page; 446pp; English

tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the renal toxicity of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database effect of a compound. electronic did not described The invention relates to a novel form part in the specification. NOTE: The sequence data for this orm part of the printed specification, but was obtained c format directly from the World Intellectual Property The method method of predicting at least one toxic comprises a gene expression profile of a patent in õ of a õ

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                                                                       CC The invention relates to a method of predicting (the progression of) a CC toxic effect of a compound by preparing a gene expression profile of a CC kidney tissue or cell sample exposed to the compound and comparing the CC gene expression profile to a database, or detecting the level of gene(s) CC expression in a tissue or cell sample exposed to the compound, where CC differential gene expression compared to a control indicates a toxic CC effect (toxicity progression). The method is useful for predicting (the progression of) at least one toxic effect of a compound. The genes are CC useful as toxicity markers in drug screening and toxicity assays. The CC methods are useful for predicting the likelihood that a compound or test agent will induce various specific kidney pathologies, such as nephritis, CC kidney necrosis, glomerular and tubular injury, or focal segmental CC glomerulosclerosis. The methods are useful for determining the similarity of a toxic response to one or more individual compounds and for CC predicting or elucidating the potential cellular pathways influenced, CC induced or modulated by the compound or test agent. The kit is useful for predicting the progression of renal disease states, for identifying genes CC that show promise as new drug targets and for greening knewly and newly the states are considered as the compound.
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that show promise as new drug targets and for screening known and newly designed drugs. This sequence corresponds to a gene marker used in the method of the invention. (Note: The sequence data for this patent did no form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicting (the progression of) a toxic effect of a compound, for monitoring the progression of renal disease states, comprises preparing a gene expression profile of a kidney tissue or cell sample exposed to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mendrick DL,
Elashoff M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO 1503; 266pp; English
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Pred. No. 6.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Castle A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G; 3175 T; 0 U; 0 Other
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The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct CC provides stimulation of insulin expression by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly suglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when CC fed ad libitum and prevent pathological ketogenesis and ketoacidosis, CC thus inhibiting the long-term complications of diabetes. The proporties CC differentiated hepatoma lines and insulin expression in these cells may CC disperse additional to those provided by secreted insulin, e.g. CC inhibition of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence CC represents a fragment of the rat liver pyruvate kinase glucose response CC element, used in production of the construct of the invention
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Best Local S
Matches 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 10; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
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Pred. No.
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RESULT 11
ABX15380/c
ID ABX153
                    The invention relates to an insulin regulator construct comprising a CC glucose response element (GIRE) of a liver pyruvate kinase (LPK) gene CC promoter and an insulin-sensitive element (ISE) of an insulin-like growth CC factor binding protein-1 (IGFBP-1) basal promoter. The construct is used to treat or prevent diabetic complications, to regulate insulin CC production, to modulate hyperglycaemia (without severe hypoglycaemia), to CC increase fat catabolism and to retard protein catabolism. The construct composition by glucose (but not other CC carbohydrates) and glucocorticoids and inhibition by glucagon so that a CC combination of these effects can maintain nearly suglycaemic conditions in diabetics during short-term fasting, large carbohydrate loads or when fed ad libitum and prevent pathological ketogenesis and ketoacidosis, CC thus inhibiting the long-term complications of diabetes. The properties of the construct are essentially specific for hepatocytes and well-cc differentiated hepatoma lines and insulin expression in these cells may call the construct are essentially specific for hepatocytes and well-cc differentiated hepatoma lines and insulin expression in these cells may call the construct are essentially specific for hepatocytes and well-cc atimulation of cellular protein degradation, and inhibition, or stimulation of other intracellular hormone receptors. This sequence crepresents a fragment of the rat liver pyruvate kinase glucose response constructs of the invention
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Best Local S
Matches 48
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                 used in
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Pred. No.
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                 construct
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                 of the invention
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RESULT 12
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                                                                                                                                   The invention relates to a method of modulation of expression of a DNA molecule (preferably inhibition of lipogenesis or glycolysis) that encodes a protein involved in glucose metabolism or lipogenesis in a cel which comprises contacting the cell with an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein (ChREBP). The method is useful for treating obesity, diabetes or vascular disease and modulating carbohydrate metabolism, for inhibiting lipogenesis or glycolysis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents an oligonucleotide used in the purification of ChREBP
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                               Modulation of the expression of DNA molecule that encodes involves use of an agent that induces phosphorylation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; lipogenesis; glycolysis; glucose metabolism;
carbohydrate response element binding protein; C
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                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 2;
                                                                                                                                                                                                                                                                                                                                                  dephosphorylation of
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-020312/02.
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                                                                    Local
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                                                                    Similarity
                CATGGGCGCACGGGGCACTCCCGTGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rate response element binding protein; ChREBP; obesity; diabetes; disease; carbohydrate metabolism; cardiac disease.
                                                                                                             30 BP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                        Conservative
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                                                                                                           A; 11 C; 11 G; 5 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
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                                                                 58.8%;
                                                                                                                                                                                                                                                                                                                                                  carbohydrate response
                                                                                                                                                                                                                                                                                                                      64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
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Pred. No.
                                                                    Score 30;
Pred. No.
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
30
                                                                   0.65;
                                                                                   DB 12;
                                                                                                           U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1e-07
                                                                                                                                                                                                                                                                                                                                                  element binding
                                                       <u>..</u>
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                                                                                Length 30;
                                                        Indels
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                                                     Gaps
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RESULT 13 ADE83567/c

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RESULT 14
ADE83566
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                              molecule (preferably inhibition of lipogenesis or glycolysis) that encodes a protein involved in glucose metabolism or lipogenesis in a ce which comprises contacting the cell with an agent that induces phosphorylation or carbohydrate response element binding protein (ChREBP). The method is useful for treating obesity, diabetes or vascular disease and modulating carbohydrate metabolism, fo inhibiting lipogenesis or glycolysis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents a L-pyruvate kinase carbohydra
        ds; lipogenesis; glycolysis; glucose metabolism;
carbohydrate response element binding protein; ChREBP; obesity; diabetes;
vascular disease; carbohydrate metabolism; cardiac disease;
                                                              L-pyruvate kinase carbohydrate response element
                                                                                                                      ADE83566;
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; SEQ ID NO 4; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulation of the expression of DNA molecule that encodes protein involves use of an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; lipogenesis; glycolysis; glucose metabolism; Chrebp; obesity; diabetes;
carbohydrate response element binding protein; Chrebp; obesity; diabetes;
vascular disease; carbohydrate metabolism; cardiac disease;
                                                                                                                                               ADE83566 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-020312/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uyeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001; 2001US-0329834P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003124590-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-pyruvate kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2002; 2002US-00272206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L-pyruvate kinase carbohydrate response element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE83567 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYED/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                       27;
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                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                        element.
                                                                                                                                                                                                                                          GGGCGCACGGGGCACTCCCGTGGTTCC 30
                                                                                                                                                                                                                                                                                                                               27
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                                                                                                                                                                                                                                                                       Conservative
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                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                 52.9%;
                                                                                                                                                                                                                                                                                                                             11 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a method of modulation of expression of a DNA
                                                                                                                                               ВP
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                                                                                                                                                                                                                                                                                  Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                            G;
                                                                                                                                                                                                                                                                                                                                                                  represents a L-pyruvate kinase carbohydrate
                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                 Length 27;
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                                                                                                                                                                                                                                                                    Gaps
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RESULT 15
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ID ADE83
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetes or vascular disease and modulating carbohydrate metabolism, for inhibiting lipogenesis or glycolysis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents a L-pyruvate kinase carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of modulation of expression of a DNA molecule (preferably inhibition of lipogenesis or glycolysis) that encodes a protein involved in glucose metabolism or lipogenesis in a cwhich comprises contacting the cell with an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein (Chreb). The method is useful for treating obesity,
                                                                                                                                                        ss; lipogenesis; glycolysis; glucose metabolism; carbohydrate response element binding protein; ChREBP; obesity; diabetes; vascular disease; carbohydrate metabolism; cardiac disease; gel shift assay.
                                                                                                                                  Unidentified
                                                                                                                                                                                                                          ChREBP gel shift assay gene sequence
                                                                                                                                                                                                                                                       29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulation of the expression of DNA molecule that encodes protein involves use of an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein
(UYED/) UYEDA K.
                       16-OCT-2001; 2001US-0329834P
                                                   16-OCT-2002; 2002US-00272206
                                                                                                       US2003124590-A1
                                                                                                                                                                                                                                                                                                          ADE83614 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response element.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-020312/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001; 2001US-0329834P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 BP; 2
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Search completed: September 1, 2005, 00:34:35 Job time: 60.0797 secs
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                                                                                                                                                                 Query Match 51.0%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 15; Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                            The invention relates to a method of modulation of expression of a DNA molecule (preferably inhibition of lipogenesis or glycolygis) that encodes a protein involved in glucose metabolism or lipogenesis in a cell which comprises contacting the cell with an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein (chREBP). The method is useful for treating obesity, diabetes or vascular disease and modulating carbohydrate metabolism, for inhibiting lipogenesis or glycolygis and modulating expression of a DNA molecule that encodes a protein involved in glucose metabolism or lipogenesis in a cell (e.g. human liver cell) and for treating cardiac disease. The present sequence represents a ChREBP gel shift assay gene
                                                                                                                                                                                                                                                       Sequence 26 BP; 2 A; 9 C; 11 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulation of the expression of DNA molecule that encodes protein involves use of an agent that induces phosphorylation or dephosphorylation of carbohydrate response element binding protein.
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Cgnn2 6/ptodata/2/pubpna/US08 NEW PUB.seq: *
/ Cgnn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq: *
/ Cgnn2 6/ptodata/2/pubpna/US09 NEW PUB.seq: *
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US-09-972-916A-3

US-09-972-916A-5

US-09-972-916A-6

US-09-972-916A-6

US-10-188-934-36

US-10-152-319A-2150
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Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 36, Appl
Sequence 2150, Ap
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	23.8	•	23.8	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24.4	24.4	24.4	24.4	24.4	24.4	24.6	24.6	24.6	26	27	27	w	36.6
46.7	٠	•	46.7	47.1		47.1	٠	•	47.1	٠	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	47.1	٠		•	٠	٠	٠	٠		47.8		48.2		œ	51.0	52.9	52.9	58.8	71.8
27	27	27	27	2046	2046	2046	2046	2046	2046	2046	2046	1905	1595	1579	1546	1498	1333	1311	1191	1188	1188	525	209	3511	3138	13	3138	3138	3138	55001	55001	55001	26	27	27		31703
15	15	15	15	14	14	11	10	10	9	9	9	21	9	14	15	9	15	15	18	24	14	16	16	20	22	20	18	17	9	21	17	17	15	15	15	15	17
272-206-	0-272-206-	-10-272-206-	-10-272-206-	-10-103-313-	-10-073-865	-09-764	-09-764-886-	09-989-442-	US-09-764-853-875	US-09-764-886-84	US-09-764-893-130	US-10-505-486-226	US-09-798-710-1	US-10-073-885-11	US-10-225-567A-584	US-09-826-508-37	US-10-017-161-1921	-10-029		-11-086-846-	-10-094-417-	-10-02	-10-02	US-10-723-860-4919	US-10-756-149-213	US-10-723-860-176	US-10-342-887-909	US-10-172-118-909	09-880-107-171	-10-991	-10-348	-160	US-10-272-206-51	-10-272-206-	-10-272-20	-10-272-206-2	US-10-085-117-172
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US-09-972-916A-1
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                                                                                                                                                                                                                                                                  Sequence 1, Application US/09972916A
Patent No. US20020107199A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CUCRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                   NUMBER OF SEQ
SEQ ID NO 1
                                                                                           Query Match
Best Local S
                                                                         Matches
                                                                                                                                                                        TYPE: DNA
ORGANISM: Rattus
FEATURE:
                                                                                                                                                                                                                                 LENGTH: 51
                              1 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                                             Similarity
CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 51
                                                                         100.0%; silarity 100.0%; F
Conservative 0;
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                                                                         Score 51; DB 9; ]
Pred. No. 8.1e-09;
); Mismatches 0;
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US-09-972-916A-5/c
; Sequence 5, Application US/09972916A
; Patent No. US20020107198A1
; GENERAL INFORMATION:
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Best Local S
Matches 51
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Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
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APPLICANT: Thule, Peter M.
APPLICANT: Thule, GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
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LENGTH: 270
SEQ ID NO 5
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                              APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
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                     NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity
Thes 51; Conserv
                                                                                      ; LENGTH: 13011
; TYPE: DNA
; ORGANISM: Rattus
US-10-388-934-36
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/10388934 Publication No. US20040005547A1 GENERAL INFORMATION:
                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 36
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
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Patent No. US20020107198A1
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                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 02005336.9 PRIOR FILING DATE: 2002-03-14 PRIOR APPLICATION NUMBER: 02015657.6 PRIOR FILING DATE: 2002-07-17 NUMBER OF SEQ ID NOS: 862
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Lau
APPLICANT: Wolf, Detlef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/972,916A CURRENT FILING DATE: 2001-10-10 PRIOR APPLICATION NUMBER: US 60/239,113 PRIOR FILING DATE: 2000-10-11
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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TYPE: DNA
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Wolf, Detlef
                100.0%; ilarity 100.0%; Conservative 0
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llarity 100.0%;
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Pred. No. 5.7e-09;
                Score 51; DB 17;
Pred. No. 3.2e-09;
; Mismatches 0;
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Pred. No. 5.8e-09;
); Mismatches 0;
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                                                 Length 13011;
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Best Local S
Matches 51
                                                                                                                                                    Sequence 172, Application US/10085117 Publication No. US20030232334A1 GENERAL INFORMATION:
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                  APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
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APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
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PRIOR TILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR APPLICATION NUMBER: US 60/303,810
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PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Genbank Accession No. X05684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/303,810 FILING DATE: 2001-07-10 APPLICATION NUMBER: US 60/303,807 FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                              3021 CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 3071
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                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 51; DB 18; 100.0%; Pred. No. 3.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See File Wrapper or
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 13011;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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NUMBER: FAS SOFTWARE: FAS ; SEQ ID NO 3 FENCTH: 27

ORGANISM: Artificial Sequence

TYPE: DNA

NUMBER OF SEQ ID NOS: 66

FastSEQ for Windows Version 4.0

GENERAL INFORMATION:
APPLICANT: KOSAKU UYGEA
APPLICANT: KOSAKU UYGEA
TITLE OF INVENTION: CARBOHYDRATE RESPONSE ELEMENT BINDING
TITLE OF INVENTION: PROTEIN AND USES THEREOF
FILE REFERENCE: A34675 090495.0240
CURRENT APPLICATION NUMBER: US/10/272,206
CURRENT APPLICATION NUMBER: 60/329,834
PRIOR APPLICATION NUMBER: 60/329,834
PRIOR APPLICATION NUMBER: 60/329,834

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                                    RESULT 10
US-10-272-206-3
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US-10-272-206-2
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Sequence 3, Application US/10272206 Publication No. US20030124590A1
                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10272206
Publication No. US20030124590A1
GENERAL INFORMATION:
APPLICANT: KOBAKU Uyeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 172
                                                                                                                                                                                    Matches
                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CARBOHYDRATE RESPONSE ELEMENT BINDING TITLE OF INVENTION: PROTEIN AND USES THEREOF FILE REFERENCE: A34675 090495,0240
CURRENT APPLICATION NUMBER: US/10/272,206
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/329,834
PRIOR FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: variation
LOCATION: (1)...(31703)
OTHER INFORMATION: n = any nucleotide
                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Oligonucleotide
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 31703
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                                                                                                                                              1 CATGGGCGCACGGGCACTCCCGTGGTTCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCCAGTGTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 71.8%;
Similarity 90.7%;
                                                                                                          CATGGGCGCACGGGGCACTCCCGTGGTTCC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCTGGCATA 2078
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                   58.8%; Score 30; DB 15; 100.0%; Pred. No. 0.31;
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Pred. No. 0.00041;
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RESULT 12
US-10-272-206-51
US-10-272-206-51, Application US/10272206
; Sequence 51, Application US/10272206
; Publication No. US20030124590A1
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US-10-272-206-4/c
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                                                                                                                       SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KOBARU Uyeda
TITLE OF INVENTION: CRABOHYDRATE RESPONSE ELEMENT
TITLE OF INVENTION: PROTEIN AND USES THEREOF
FILE REFERENCE: A34675 090495.0240
CURRENT APPLICATION NUMBER: US/10/272,206
CURRENT FILING DATE: 2002-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CARBOHYDRATE RESPONSE ELEMENT BINDING TITLE OF INVENTION: PROTEIN AND USES THEREOF FILE REFERENCE: A34675 090495.0240
CURRENT APPLICATION NUMBER: US/0.272,206
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: 60/329,834
PRIOR APPLICATION NUMBER: 60/329,834
PRIOR FILING DATE: 2001-10-16
NUMBER OF SEO ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 27
   Matches
                                  Query Match
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APPLICANT: Kosaku Uyeda
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Best Local :
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PRIOR FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                         OTHER INFORMATION:
                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Oligonucleotide from wild type pyruvate kinase OTHER INFORMATION: carbohydrate response element (ChRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Oligonucleotide from wild type pyruvate kinase OTHER INFORMATION: carbohydrate response element (ChRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 27
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                    Local
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 l Similarity
26; Conserv
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27; Conserv
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51.0%; Score 26; DB llarity 100.0%; Pred. No. 8. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                         Oligonucleotide
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100.0%; Fred. No.
tve 0; Mismatches
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                 DB 15;
. 8.7;
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                                  Length 26;
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RESULT 15
US-10-991-147-4
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US-10-348-750-4
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US-10-160-497-4
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Sequence 4, Application US/10991147
Publication No. US20050096292A1
GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10348750 Publication No. US20030225019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Susan M. Freier
APPLICANT: Kenneth W. Dobie
APPLICANT: Erich Koller
TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH1 EXPRESSION
                                                                                                                                                                                                                            Best Local Similarity Matches 33; Conserv
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOTCH1 INHIBITORS FOR INDUCING APOPTOSIS FILE REFERENCE: ISPH-0729
CURRENT APPLICATION NUMBER: US/10/348,750
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 10/160,497
PRIOR PILING DATE: 2002-02-20
RUMBER OF SEQ ID NOS: 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Susan M. Freier APPLICANT: Kenneth W. Dobie APPLICANT: Erich Koller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/160,497
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: RTS-0386
                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 55001
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 55001
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                                                                                                                                                                                                                                              Score 24.6;
Pred. No. 7.
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5.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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 212.4
1212.4
188.4
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length: 2000000000
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Match Length DB
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97.0
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BC078889

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MMILGF
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                                                                            AX401932 Sequence
AX827271 Sequence
M58634 Rat IGF bin
AX163782 Sequence
L22979 Rat insulin
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M74587 Human insul
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15.5	15.5	15.6	15.6	15.6	15.6	16.0	16.0	16.0	16.0	16.0	16.0	16.3	16.8	16.8	16.8	17.3	17.3	17.3	20.3		23.0	27.0	27.0	27.0	27.8
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L36088 Rattus norv	BC083173 Rattus no	AF069489 Homo Bapi	AY326105 Rattue ex	AB096856 Rattue ta	AB033706 Diplothri	AC034102 Homo sapi	AY056018 Homo sapi	L31573 Human sulfi	CQ721974 Sequence	BC065193 Homo sapi	BV184757 sqnm14591	AE016922 Chromobac	BX640447 Bordetell	BX640427 Bordetell	BX640428 Bordetell	AX348680 Sequence	AX345899 Sequence	AX251887 Sequence	M89791 Rattus norv	G67173 IGFBP1 5'A	M23592 Human insul	AC148834 Pan trogl	AC146117 Pan trogl	AC146152 Pan trogl	AC091524 Homo sapi

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Original source text: Rattus norvegicus (strain Sprague-Dawley)
male adult liver DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus insulin-like om 84488
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Mammalia; Eutheria; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                      /tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Rat Genome Sequencing Consortium
                                                    Direct Submission
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                    (bases 1 to 185148)
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norvegicus clone CH230-97018,
3 unordered pieces.
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3, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 135613 bases at least Q30
Consensus quality: 140849 bases at least Q30
Consensus quality: 145680 bases at least Q20
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Center clone name: CH230-97018
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X67493
X67493.1 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-1992) R.A. Taub, Univ. of Pennsylvania, Howard Hughes Medical Institute, Clinical Research Bldg., Room 475, 422 Curie Boulevard, Philadelphia, PA 19104-6145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1363)
Mohn, K.L., Waddle, J.R. and Taub, R.
Comparison of mouse and human IGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mohn,K.L., Bucan,M. and Taub,R. Structure and localization of the IGFBP-1 gene and its expression during liver regeneration Hepatology 19 (3), 656-665 (1994) 94164648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 1363)
Lee,J., Greenbaum,L., Haber,B.A., Nagle,D., Lee,V., Miles,V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insulin-like growth
Mus musculus (house
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        boundaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1363)
                                                                                                                                                                                                                                                                                                       /cell_line="NIH 3T3"
/cell_type="fibroblast"
/clone_lib="genomic, lamb
/dev stage="embryo"
500. -.508
                                                                                                                                                                   sequences"
764. .768
792. .1336
                                                                                                  /note="mRNA
964. .>1336
          /codon_start=1
/product="insulin-like growth
/protein_id="CAA49832.1"
/db_xref="GI:52700"
/db_xref="GOA:P47876"
                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
/mol_type="genomic DNA"
/strain="NIH Swiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                     'number=1
                                                                                                                                                                                                                       note="Caat
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="JW2.1"
db_xref="UniProt/Swiss-Prot:P47876"
                                                                                                                                                                                                                                                                                         note="AP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:52699
                                                                                                                                                                                                                                                       note="insulin-responsive element"
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                                                                                                                   cap site"
                                                                                                                                                                                                                                                                                         consensus
                                                                                                                                                                                                                       box with APF, HNF and NF-El consensus
                                                                                                                                                                                                                                                                                                                                         lambda
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RESULT 4
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TITLE
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Best Local
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                                                                                source
                                                                                                                                                                                                                                                          AL Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
   humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
   On Apr 12, 2002 this sequence version replaced gi:19847866.
   During sequence assembly data is compared from overlapping clones.
   Where differences are found these are annotated as variations
   together with a note of the overlapping clone name. Note that the
   variation annotation may not be found in the sequence submission
   corresponding to the overlapping clone, as we submit sequences with
   only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
   regions were either double-stranded or sequenced with an alternate
   chemistry or covered by high quality data (i.e., phred quality >=
   30); an attempt was made to resolve all sequencing problems, such
   as compressions and repeats; all regions were covered by at least
   one plasmid subclone or more than one M13 subclone; and the
   assembly was confirmed by restriction digest. The following
   abbreviations are used to associate primary accession numbers given
   in the feature table with their source databases: Em:, EMBL; Sw:,
   SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP
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                                                                                                                                                  constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                  database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oliver, K.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG.
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/organism="Mus musculus
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
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                                                                                                     Location/Qualifiers
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92.5%;
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Pred. No. 4.1e-46;
0; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                          Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC013345 1569 bp mRNA linear ROD Mus musculus insulin-like growth factor binding protein (cDNA clone MGC:14075 IMAGE:4161889), complete cds.
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                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                        Contact: MGC help desk
                                                                                                                          NIH-MGC Project URL: http://mgc
                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 1569)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACTGCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
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/clone_lib="RPCI-23"
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92.5%;
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Pred. No. 4.
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                                                                                                                                .nci.nih
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FEATURES

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AUTHORS
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Best Local Similarity 92.8
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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Sequence
AX401932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 18 Row: i Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Molecular toxicology modeling Patent: WO 0210453-A 1608 07-FEB-2002;
                               Mendrick, D.,
Elashoff, M.R.
                                                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                        AX401932.1 GI:21338112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                  CACACGGCCATCTGCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCCAGCCAGGATGGTCCACTGCCCGGCCGAGACACAAACCCCAGCGAGCATTGAACACTG 163
                                                                                                                                                                                                                                                                                                                                                         CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGCAGCCAGCATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="insulin-like growth factor binding protein 1"
/protein_id="AAH13345.1"
/protein_id="AAH13345.1"
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/db_xref="GI:5426483"
/db_xref="MGI:96436"
/db_xref="MGI:96436"
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/translation="MEDEFLTV/SWPFLIILSFQIGVAAGAPQPWHCAPCTAERLGLCP
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GGACVPEPAARATSTLSSSQHEERKAAVVSADELSESPEMTEEQLLDSFHLMAPSRED
QPILMMAISTYSSMRARBIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                            1608 from Patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
/db_xref="MGI:96436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="Igfbp1"
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|clone="MGC:14075 IMAGE:4161889"
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strain="FVB/N"
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                                                    Porter, M.W.,
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92.8%;
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Pred. No. 9e-19;
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L WO0210453.
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                                                    Johnson, K.R.,
                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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                                                              N Rat IGF binding protein-1 (rIGFBP-1) mR 4 M58634 M58634 I GI:204732 IGF binding protein-1 Rattus norvegicus (Norway rat) M Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5 from Patent EP1344834.
AX827271
Mohn, K.L., Melby, A.E.,
                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                            Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
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             (bases 1 to 1500)
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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/mol type="unassigned DNA"
/mb type="10116"
/mb xref="reaxon:10116"
/noTe="EMBL/GenBank Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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98.7%;
                                          Chordata;
Rodentia;
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Pred. No. 3.7e.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Score 76.4; DB 6;
Pred. No. 3.7e-12;
D; Mismatches 1;
Tewari, D.S.,
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                                          Craniata; Vertebrata; I
Sciurognathi; Muridae;
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Laz,T.M.
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                                                                                                                                              mRNA,
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                                                         Euteleostomi;
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                                             Murinae;
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is rapidl
Mol. Cell
91141487
                                                                                                                                                                                                      Gould-Rothberg, B.E., Dipippo, V.A., Ramseh, T.M. and Gerwein, R.W. Method of identifying toxic agents using nsaid-induced differential gene expression in liver
                                                                                                                                                                                 Curagen
                                                                                                                                                                                             Patent:
                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Original
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e gene encoding rat insulinlike growth factor-binding protein rapidly and highly induced in regenerating liver
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                              WO 0138579-A 46 31-MAY-2001;
Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                         46
                                                                                                          /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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235. .
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QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
160. .234
                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="IGF binding protein-1"
/protein_id="AAA41380.1"
/db_xref="GI:204733"
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                                                        34.9%;
98.7%;
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Patent WO0138579
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                                       Score 76.4; DB 6; Pred. No. 3.7e-12; n. Mismatches 1;
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No. 3.7e-12;
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Lacson, R., Oehler, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTICCGCTACTATCTA 78
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               4090.
                                                        3003.
                                                                                2874. .3002
/gene="IGFBP-1"
  number=4
                         number=3
                                         gene="IGFBP-1"
                                                                                                                         2035. .2873
'gene="IGFBP-1"
                                                                    number=3
                                                                                                                                                                850. .2034
gene="IGFBP-1"
                                                                                                                                                                                                         gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                    gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                            number=1
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                                                                                                           number=2
                                                                                                                                                    number=2
                                                                                                                                                                                            number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
                                                                                                                                                                                                                                                                                                                                              codon_start=1
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Lacson,R., Oehler,D., Yang,E., Goswami,R. and Unterman, Dideoxy sequencing and structural analysis of the rat i growth factor binding protein-1 gene Blochim. Biophys. Acta 1218 (1), 95-98 (1994)
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insulin-like growth factor binding
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RATIGFBA 5001 bp DNA linear ROD 30-NOV-1 Rat insulin-like growth factor binding protein-1 (IGFBP-1) gene, complete cds. L22979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Nov 30, 1995 this sequence version replaced gi:385167
Original source text: Rattus norvegicus (strain Sprague-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                              /product="insulin-like growth factor binding protein"
/protein id="AAA82581.1"
/db.xref="01:1098473"
/translation="MPEFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP
/translation="MPEFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP
PVPASCPEISRPAGCGCCPTCALPLCAACGVATAACAQCLSCRALPGEBRPLHALTRG
OGACVLEPAAPATSSLSGOHEEAKAAVASEBDELABSPEMTEBOLLDSFHLMAPSTED
OPILWNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
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/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dev stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="liver"
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RESULT 11
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Best Local Similarity
Matches 143; Conserv
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                                              491 TAACTTTCTAGTCCAAGTGGAGTGAACCGCGCCCTTTATAAGGCAAGGGCTGCACCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1507)
Li,Y., Klimanis,D. and Hallenbeck,J.M.
Cloning and characterization of insulin-like
protein 1 (IGFBP-1) from thirtean-lined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermophilus tridecemlineatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermophilus tridecemlineatus insulin-like protein 1 (IGFBP1) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-FEB-2004) StrokeBranch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermophilus tridecemlineatus (thirteen-lined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY560836.1 GI:45505308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                          CAGGAGCAAAACTTATTTTGAACACTGGGCTCCTAGCACGCCGCGCTGGCAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTTCCGCTACTAGCTA 214
                                                                                                                                         CACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTTCCGCTACTATCTA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y., Klimanis, D. and Hallenbeck, J.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 1507)
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
                                                                                                                                                                                                                                                            /product="insulin-like growth factor binding protein 1"
/protein id="AAS67029.1"
/db xref="GI:4550309"
/db xref="GI:4550309"
/translation="MPEVPAAGLMPFLLLLAVQVSTVASSTQPWHCAPCSAEKLALCP
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OPILWMAISTYKSMRAREMADIKKWKQPCREELYKVLERLAKAQQKAGEEIXKFYLPN
                                                                                                                                                                                                                                                    CNKNGFYHSKQCETSLDGEAELCWCVYPWSGRRIPGSLEIRGDPNCHQYFNVQN"
                                                                                                                                                                                                                                                                                                                                                                                          /gene="IGFBP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4222.
                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="IGFBP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Spermophilus
                                                                                                                                                                                     34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       xref="taxon:43179"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.9%;
                                                                             -GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 3.7e-12;
0; Mismatches 1
                                                                                                                                                                                      Score 76.2; DB 10;
Pred. No. 4.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1507 bp
                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ground
                                                                                                                                                                                                     Length 1507;
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AUTHORS
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BC078889
                                                                                                                                                                                                                                                                                                                              COMMENT
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PUBMED
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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                                              source
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Strauberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buctow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Glbbs, R. A.,

Vallalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Glbbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

D. 12477023 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 AAGCATCGTGCACTGCCCACGGCGACTCAGAATTGGACACCTATCAA-----GCCACTGC 605
                                                                                                                                                           Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 184 Row: e Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6981079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web alte: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Director MGC Project.
Direct Submission
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC078889.1 GI:50927646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCTGCCCAGAGAGCTGTGACCACCACTTC 202
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/organism="Rattus norvegicus"
/mol_type="mRNA"
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                                                                                                                         .1510
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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AY095345
                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                      FEATURES
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Best Local S
Matches 66
                                                                                                                               JOURNAL
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                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                       Direct Submission
Submitted (11-APR-2002) Department of Obstetrics and Gynecology,
University of Illinois at Chicago, 820 S. Wood, Chicago, IL 60612,
                                                                                                                                                                                                 1 (bases 1 to 3886)
Kim, J.J., Taylor, H.S., Akbas, G.E., Foucher, I., Trembleau, A.,
Jaffe, R.C., Fazleabas, A.T. and Unterman, T.G.
Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells
Biol. Reprod. 68 (1), 24-30 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
                                                                                                    USA
                                                                                                                                                        2 (bases 1 to 3886)
Kim, J.J., Jaffe, R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                  AY095345

AY095345

Papio anubis insulin-like growth factor binding protein-1 (IGFBP-1)
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithe
                                                                                                                                                                                                                                                                                                                                                                             AY095345.1 GI:20853764
                                                                                                                                                                                                                                                                                         Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                   Papio anubis
                                                                                                                                                                                                                                                                                                                                                Papio anubis (olive baboon)
                                                                                                                                                                                      12493691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCACCACTTCCGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAGCTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         partial cds.
              \frac{\text{db } xr}{3655}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="insulin-like growth factor binding protein protein id="AAH78889.1"
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/db_xref="H_OCUSID:25685"
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/gene="IGFBP-1"
              /mol_type="genomic DN
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<3655. .>3886
                                                       organism="Papio anubis
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDFNCHQYFNVQN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="synonyms: IGFBA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Igfbp1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:93595 IMAGE:7129185"
/tlssue_type="Kidney, rat (Brown
/clone_lb="WIH_MGC_236"
/lab_host="DH10B"
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Pred. No. 7.9e-09;
0; Mismatches 1
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Primer B:
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Homo sapiens
                                                        Buffer:
                                                                                                                                                                       Protocol:
                                                                                                                                                                                  STS size: 448
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                                                                                                                                                                                                                                                                                                                                                Unpublished
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Primer:
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MgCl2:
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3539 CACCCTCCCAGAGAGCACTGGCCACCGCTCC 3569
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International Agency for Research
150, cours Albert-Thomas, F-69372
Tel: +33-4-72738698
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Cox,D.G., Boillot,C. and Canzian,F. Genome Survey
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                                                                                                                                                                                                                                                                                     Email: canzian@iarc.fr
                                                                                                                                                                                                                                                                                                                                                                                               Contact: Federico Canzian
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GGGTGACCTCCGAGCACG
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Best Local Similarity 66.5
Matches 141; Conservative
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171
                                593
                                                             112 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG 170
                                                                                                   533 TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
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Location/Qualifiers
1. 6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2394 from Patent WO0229103.
AX409747 GI:21442452
CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202
                                GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCGCCCCC
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/mol type="unassigned DNA"
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/noCe="EMBL/GenBank Accession No. M74587"
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/clone_lib="Human"
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Pred. No. 1.9e-07;
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Search completed: September 1, 2005, 03:26:45 Job time : 1371.59 secs

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Maximum Match 100%
Listing first 45 summaries
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34239544 segs, 19032134700 residues
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GenCore version (c) 1993 - 2005
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AII530313
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CA478518
AII790802
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AII798304
AII785039
CO573026
CV127049
CV573026
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AI196314
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Compugen Ltd.
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CA478518 AGENCOURT
A1790802 uk28b10.y
A1528304 ui95g10.y
A1528304 ui95g10.y
A1796154 ui69d08.y
A17965039 ui73a06.y
CO573026 AGENCOURT
CV127049 AGENCOURT
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AI530146 ui89f09.y
AI530146 ue31e07.y
AI098594 ue31e07.y
AI530313 ui91f01.y
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Query Match
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1013)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9443 row: j column: 02
High quality sequence stop: 581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF236974 1013 bp mRNA linear EST 14-NOV-2000 602026605F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4161889 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                       /db_xref="taxon:10090"
/clone="IMGG:4161889"
/lab host="PH108 (T1 phage-resistant)"
/clone_lib="NCI CGAP_Li9"
/clone_lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                   mol_type="mRNA"
strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers,
                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                        44.8%;
Score 98.2; DB 2;
Pred. No. 1.2e-18;
0; Mismatches 8;
                                             Length 1013;
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104 TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTG 163

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BY783538.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Crai
Mammalia; Eutheria; Rodentia; Scii
1 (bases 1 to 310)
Carninci, P., Waki, K., Shiraki, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY783538 RIKEN full-length enriched, 17.5 days embryo Mus musculus cDNA clone L930176D05 5', mRNA sequence.
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22703353
                                                                                                                                                                 Similarity
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TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                   ATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC 175
                                                             ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                               /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5
                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="L930176D05"
                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                               40.1%;
92.9%;
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Pred. No. 1.3e-15;
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Sciurognathi; Muridae; Murinae;
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d, 17.5 days embryo whole body
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Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
LGenome Res. 13 (6B), 1273-1289 (2003)
176
                                                                                                                      116 ATGGTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC
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92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.jp/) for
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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BY794229 RIKEN full-length enriched, 17.5 days embryo
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1 (bases 1 to 331)
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TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                               ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC 61
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                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="kIKEN full-length enriched, 17.5 days embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="L930292H24"
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                                                                                                                                                                                  Score 87.8; DB 6;
Pred. No. 1.3e-15;
D; Mismatches 7;
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d, 17.5 days embryo whole body
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                                                                                                                                                                                                                                            Length 331;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzawa, K., Arakawa, T., Ishii, Y., Konno, H., Shibata, K., Itoh, M., Sugahara, Y., Saito, R., Osato, N., Pukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aldinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Targeting a Complex transcriptome: the construction of the mouse Genome Res. 13 (AR)
                                                                                                                                                                                                                          62
                 401 bp mRNA linear EST 02-
ui78h05.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888569 5' similar to gb:x81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE); mRNA sequence
                                                                                                                                                                                                                                                                                                                      N
insulin-like
AI785818
                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 354)
Carninci, P., Waki, K., Shiraki, T.,
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BY771317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 13 (6B), 1273-1289 (2003)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                       TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                                                                                                                                                                                                                                                TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                                                                                                                                                                                                                                                   ATGGTCCACTGCCCGCGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
                                                                                                                                                                                                                                                                                                                                                                  ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC 175
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 bp mRNA linear EST 23-MAR-2)
RIKEN full-length enriched, 17.5 days embryo whole body
ulus cDNA clone L930052G15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole body"
/dev stage="17.5 days embryo"
/clone lib="RIKEN full-length enriched, 17.5 days embryo
whole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930052G15"
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Pred. No. 1
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L.4e-15;
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RESULT 6
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All963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_ESTs: ui78h05.xl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 401)
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EST.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); lst = 2: DraIII (CACCATGTG); lst = 1: DraIII
(CACTGTGTGT); Site_2: DraIII (CACCATGTG); lst = 1: DraIII
(CACTGTGTGTG); lst = 1: DraIII (CACCATGTG); lst = 1: DraIII alpha was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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Pred. No. 2.8e-15;
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AI530146
108 DP WIGHER
11895(19.91 Sugano mouse liver mlia Mus musculus cDNA clone
11MAGE:18896(19.5' similar to gb:M59316 rna1 INSULIN-LIKE GROWTH
FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus
mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1810
Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.
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                                                                                                                                                                                                                                                                                                                                         TGGTCCACTGCCCGCGGAGCACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Sugano mouse liver mlia"
/note="Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL"
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Pred. No. 2.9e-15;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                117 TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCCATCT 176
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AI530146
AI530146.1
                 A1098594 mRNA linear EST 20-ue31e07.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 314 400 10.10
Email: mouseest@wattson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                  GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                                                                                                                                                                                                                                                  TGGTCCACTGCCCGCGGAGACACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Sugano mouse liver mila"
/note="Organ: liver; Vector: pMEIBS-FH3; Site 1: DraIII
(CACCTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEIBS-FH3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/clone="IMAGE:1889609"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86.8; DB 1;
Pred. No. 3.1e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 706;
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                                                                                                 EST 20-AUG-1998
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RESULT 9
AI530313
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Best Local S
Matches 91
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI098594.1 GI:3448119
EST.
Mus musculus (house mouse)
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/note="Torgan: liver; Vector: pMELBS-FL3; Site 1: DraIII (CACCATGTGG); Site 2: DraIII (CACCATGTG); lst Strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pMELBS-FL3 vector (5' site CACTGTGG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTGTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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Pred. No. 3.
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RESULT 10
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A1529939
799 bp mRNA linear EST 18-MAR-1: u187C09.yl Sugano mouse liver mlia Mus musculus CDNA clone IMAGE:189392 5' similar to gb:m59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
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The WashU-NCI Mouse EST Project 1999
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 785)
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AI530313.1
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//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME185-FL3; Site 1: Draili (CACCATGTG); lst strand cDNA
(CACTGTGTG); Site 2: Draili (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a Draili adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct Draili sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/strain="C57BL"
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92.9%;
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Pred. No. 3.2e-15;
D; Mismatches 7;
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RESULT 11
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AGENCOURT 10789306 NIH MGC 152 MUS
IMAGE:6766752 5', mRNA sequence
CA478518
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Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                 CA478518
CA478518.1
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Location/Qualifiers
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//Clone_lib="Sugano mouse liver mlia"
//Clone_Torgan: liver; Vector: pwEl8S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
{ATCTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pwEl8S-FL3
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constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/clone="IMAGE:1889392"
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                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 848)
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uk28b10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1970299 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri
1 (bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/db_xref="taxon:10090"
/clone="IMAGE:6766752"
/lab host="DH10B (phage-resistant)"
/clone lib="NH1 MGC_152"
/clone lib="NH1 MGC_15
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Pax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 852)
Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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//Clone lib="Sugano mouse mkia"
//Clone lib="Sugano ligo(dT) primer
//Clone lib="Sugano ligo(dT) primer
//Clone lib="Sugano ligo(dT) primer
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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                 TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All196154 linear EST 14-OCT-19 MRNA linear EST 14-OCT-19 MIG-0008, yl Sugano mouse lives mia Mus musculus cDNA clone IMAGE:1887663 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina 1 (bases 1 to 605)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubgeisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theiaing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:974534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                 The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI196154.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site_1: Draili
(CACCATGTGTG); Site_2: Draili (CACCATGTG); 1st strand cDNA
(CACTGTGTGG); Site_2: Draili (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a Draili adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct Draili sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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strain="C57BL"
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lab_host="DH10B"
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92.9%;
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                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 852;
                                                                                                                                                                                                                         Dietrich, N., Dubuque, T.,
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Gaps

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TITLE
JOURNAL
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Best Local
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       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M

1 (bases 1 to 380)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, F

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

The Washi-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                            AI785039 380 bp mRNA linear EST 02-ui73a06.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1888018 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                           AI785039
AI785039.1
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This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1810
Fax: 314 286 1810
  Unpublished (1999)
                                                                                                                                                                                                                                                                          Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGTCGTCT
                                                                                                                                                                                                                                                                          musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Clone libe "Sugano mouse liver mlia"
//clone libe "Sugano mouse libe "Fi3; Site libe stranded cDNA was primed with an oligo/dT) primer

[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Dralli adaptor [TGTGGCCTACATGG], digested and cloned into distinct DrallI sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra M/Mouse EST Project
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/strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                             GI:5332755
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91.8%;
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Pred. No. 9.2e-15;
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                                                                        Cardenas, M., McCann, R.,
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                                                                                             Schurk, R.,
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Best Local
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                             180 CAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 214
                                                                                                                                                   120 TCCACTGCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCC 179
61
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington Eark Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                          Similarity
CAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                    TCCACTGCCCGCGGAGACACACCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC 60
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                                                                                                                                                                                                     Conservative
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//Clone lib="Sugano mouse liver; Wector: pMB18S-FL3; Site 1: DralII
//Clone="Corgan: liver; Vector: pMB18S-FL3; Site 1: DralII
(CACCATGTGTG); Site 2: DralII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCTTTTTTTTTTTTTTTTT], double-stranded cDNA was
ligated to a DralII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DralII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG); Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dev_stage="adult"
lab_host="DH10B"
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clone="IMAGE:1888018"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                          37.5%;
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Pred. No. 6.7e-14;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      219 100.0
219 100.0
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1: /cgn2_6/ptodata/2/pubpna/US07
2: /cgn2_6/ptodata/2/pubpna/PCT_1
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/ cgn2_6/ptodata/2/pubpna/US06_NEW_PUB_seq:*
/ cgn2_6/ptodata/2/pubpna/US06_NEW_PUB_seq:*
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/ cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_seq:*
/ cgn2_6/ptodata/2/pubpna/US08_NEW_PUB_seq:*
/ cgn2_6/ptodata/2/pubpna/US08_PUBCOMB_seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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: /cgn2 6/ptcdata/2/pubpna/US09C_PUBCOMB.Beq;*
: /cgn2 6/ptcdata/2/pubpna/US09C_PUBCOMB.Beq;*
: /cgn2 6/ptcdata/2/pubpna/US10A_PUBCOMB.Beq;*
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: /cgn2 6/ptcdata/2/pubpna/US10E_PUBCOMB.Beq;*
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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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US-09-972-916A-4
US-09-972-916A-5
US-09-972-916A-6
US-09-972-916A-6
US-09-977-900A-1608
7 US-10-388-934-5
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2248.600 Million cell updates/sec
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Sequence 4, Appli
Sequence 5, Appli
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Sequence 5, Appli
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-10-221-278-3	-10-291-172-3	-10-119-428-3	-10-696	-10-972-079-8	S-10-156-761-	-10-221-613-25	6-761-13	-10-653-047	-10-363-483A-4049	-483	-10-363-345A-4049	-10-363-345A-4049	-10-282-122A-3325	-10-425-115-2833	-10-367-094	-10-072-012	-10-120-988	-292-798	-10-017-161	-10-343-903	-10-322-281	-10-437-963	-10-437-963	-10-741-600	10-741-601	-10-011-585A-76	-10-027-632-164	-10-027-632-16433	-10-739-930-546	-221-613-	-10-311-455-97	-10-893-315-16	-10-893-315-	S-10-756-149-14	-09-880-107-2393	-152-319A-	S-10-191-80
31, App	Φ	equence 34, App	equence 51,	equence 825	equence 1,	equence	equence 131	e 276	equence 404	equence 404	e 404	equence 404	equence 332	e 2833	e 169,	equence 29,	404,	equence	equence 2017	31,	equence 492,	e 7918	equence 7916	Sequence 17905, A	5746	equence 76,	equence 164336	equence 16433	equence 5461	equence 148,	equence 97	equence 160,	equence 126,	e 1484	quence 2393, Ap	Φ	equence 73, App

ALIGNMENTS

RESULT 1 US-09-972-916A-2

GENERAL INFORMATION: APPLICANT: Thule, P

Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6

Sequence 2, Application US/09972916A Patent No. US20020107198A1

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                                                                                                                                                     SEQ ID NO 2
LENGTH: 219
                                                                       Matches
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Best Local Similarity
                                                                                                                        TYPE: DNA ORGANISM: Rattus norvegicus FEATURE:
                                                                      219;
ь
                                                  1 TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA 60
                                                                       Conservative
                                                                               100.0%;
                                                                    0;
                                                                      Score 219; DB 9;
Pred. No. 1e-68;
; Mismatches 0;
                                                                                         Length 219;
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                                                                                                                         Sequence 4, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILLING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
                                                                           NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
LENGTH: 321
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LENGTH: 270
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Best Local
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TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthesized -09-972-916A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 6
                            ORGANISM: Artificial Sequence FEATURE:
               OTHER INFORMATION: Synthesized
                                                             TYPE: DNA
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Pred. No. 1.1e-68;
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Patent No. US20020107198A1
GENERAL INFORMATION:

APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
Sequence 6, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
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Best Local Similarity
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                                       PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOPTWARE: PATENTIN VET. 2.1
SEQ ID NO 1608
LENGTH:/1500
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PRIOR APPLICATION NUMBER: US 60/;
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
LENGTH: 423
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TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/303,459
ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/295,798 FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                            FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/292,336
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Pred. No. 1.2e-68;
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APPLICANT: MENDRICK, Donna
APPLICANT: MODRICK, Mark
APPLICANT: HORNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
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US-10-191-803-73
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                                                                                                                                                                                                                                                                                                                  Sequence 73, Application US/10191803 Publication No. US20040014040A1 GENERAL INFORMATION:
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Matches
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APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laux
APPLICANT: Wolf, Detlef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Publication No. US20040005547A1
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CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
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nes 77; Conserv
APPLICATION NUMBER: US 60/369,351
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Pred. No. 6.2e-17;
0; Mismatches 1;
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Pred. No. 6.
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6.2e-17;
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; OTHER INFORMATION: Genbank Accession No. US-10-152-319A-1613
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US-10-191-803-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILLING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILLING DATE: 2001-06-13
PRIOR FILLING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILLING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR APPLICATION NUMBER: US 60/303,807
                                                                                                                                           SOFTWARE: Patentin
SEQ ID NO 1613
LENGTH: 1500
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  Query Match
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Best Local Similarity
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 2221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mendrick, Don APPLICANT: Porter, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2002-05-06 NUMBER OF SEQ ID NOS: 1140
                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-04-03
                                                                                                                              TYPE: DNA
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                                                                                    FEATURE:
                                                                                                     ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/324,928 FILING DATE: 2001-09-27 APPLICATION NUMBER: US 60/330,867
                                                                                                                                                                                                                                                                   FILING DATE: 2001-11-01
APPLICATION NUMBER: US 60/330,462
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/315,047 FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/303,808 FILING DATE: 2001-07-10
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                                                                                                                                                                                       Ver.
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98.7%;
  34.9%;
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Score 76.4;
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Pred. No. 6.2e-17;
0; Mismatches 1;
                                                           NM_013144
DB 18;
Length 1500;
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US-10-756-149-1484
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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US-09-880-107-2393
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LENGTH: 6128
TYPE: DNA
GENERAL INFORMATION:
APPLICANT: AZIZ, NATASHA
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
                                                                                                                                                                                       Sequence 1484, Application US/10756149 Publication No. US20050181375A1
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Patent No. US2002014
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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0020142981A1
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66.5%;
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Pred. No. 4e-11;
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); Mismatches 1;
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AND

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Sequence 126, Application US/10893315
PUBLICATION NO. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENTITLE OF INVENTION: WITH TYPE II DIABETES ANI
TITLE OF INVENTION: WITH TYPE II DIABETES ANI
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 9173
TYPE: DNA
ORGANISM: Human
US-10-893-315-126
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US-10-893-315-126
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RESULT 13
US-10-893-315-160
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US-10-756-149-1484
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SEQ ID NO 1484
LENGTH: 6128
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Best Local Similarity
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Best Local Similarity
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                                                                                                     CCATCTGCCCAGAGAGCTGTGACCACCACTTC 202
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66.5%;
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Pred. No. 4.4e-11;
0; Mismatches 52;
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Pred. No. 4e-11;
0; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 676
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APPLICANT: DIEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR RELING DATE: 2000-06-30
PRIOR RELING DATE: 2000-06-30
PRIOR RELING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
                                                                                                         ; OTHER INFORMATION: chemically treated US-10-311-455-970
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Publication No. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
TITLE OF INVENTION: WITH TYPE II DIABETES
TITLE OF INVENTION: USES THEREOP
FILE REFERENCE: CL000786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 970, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 160
LENGTH: 9174
TYPE: DNA
ORGANISM: Human
     Matches
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CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                             FEATURE:
     Local Similarity
les 48; Conserv
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                        17.3%;
  Score 37.8; DB 15;
Pred. No. 0.0086;
0; Mismatches 17;
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Pred. No. 4.4e-11;
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RESULT 15

US-10-221-613-148/c

Sequence 148, Application US/10221613

Publication No. US20040029123A1

Publication No. US20040029123A1

APPLICANT: OLEK, ALexander

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle

FILE REFERENCE; 5013.1004

CURRENT APPLICATION NUMBER: US/10/221,613

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: PCT/EP01/02945

DE 10013847.00

DE 10013873.8

DE 10013529.7

DE 10043826.1

PRIOR FILING DATE: 2001-03-15

2000-04-06

2000-04-07

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2000-06-30
Search completed: September 1, 2005, 16:44:10 Job time: 647.824 secs
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                                                                                                                                                                                                                                                                                                     ; ORGANISM: Artificial Sequence ; FEATURE; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-613-148
                                                                                                                                                                                                                        Query Match 17.3
Best Local Similarity 73.8
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                              2000-09-01
NUMBER OF SEQ ID NOS: 428
SEQ ID NO 148
LENGTH: 7061
TYPE: DNA
                                                                            2125 TAACC 2121
                                                                                                                                                 2185 CACTAACAAAACAAACTTATTTTAAACACTCAACTCCTAACGTACGACGCTACCAATCAT 2126
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                                                                                                                                                                                                                          17.3%; Score 37.8; DB 17; 73.8%; Pred. No. 0.0086; ative 0; Mismatches 17;
                                                                                                                                                                                                                                                              Length 7061;
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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Match Length DB
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     Copyright
     GenCore version (c) 1993 - 2005
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 US-09-949-001-30
US-09-949-016-136
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US-09-949-016-11816
US-09-949-016-11816
US-09-949-016-11816
US-09-949-016-11745
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US-09-949-016-11990
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Compugen Ltd.
Sequence 30, Appl Sequence 19194, A ppl Sequence 19184, A sequence 74, Appl Sequence 71895, A sequence 11816, A ppl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11745, A sequence 11745, A sequence 11745, A sequence 11745, A sequence 16518, A sequence 16518, A sequence 16590, A sequence 169692, A sequence 1310, A sequence 13003, A sequence 1310, A sequence 1310, A sequence 1310, A sequence 1310, A sequence 1303, A sequence 1303, A sequence 1308, A sequence 1241, Appli Sequence 17016, A sequence 1701
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RESUI US-0: ; See ; Pa! ; GE! ; T	B & B & B & B & B	US-0 US-0 US-0 PP	0 00 0 0
RESULT 2 US-09-949-001-36 ; Sequence 36, Application US/09949001 ; Patent No. 682536 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED	2 CACAACCAAAACAAATTATTTGAACACGGGG	RESULT 1 US-09-949-001-30 ; Sequence 30, Application US/09949001 ; Patent No. 6825366 ; GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION FILE REFERENCE: CL000789 ; CURRENT APPLICATION NUMBER: US/09/949,001 ; CURRENT FILING DATE: 2003-01-15 ; PRIOR APPLICATION NUMBER: 60/231,323 pRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 848 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 30 ; LENGTH: 9173 TYPE: DNA ; ORGANISM: Human US-09-949-001-30 Query Match Best Local Similarity 66.5%; Pred. No. 8.8e-10; Matches 141; Conservative 0; Mismatches 52; Indels	28 29 13.2 790 3 US-08-998-416-7479 29 29 13.2 2194 4 US-09-270-767-10411 30 29 13.2 2205 4 US-09-270-767-10411 31 29 13.2 2205 4 US-09-252-991A-11217 31 29 13.2 13489 4 US-09-252-991A-11038 32 29 13.2 13489 4 US-09-949-016-15911 33 29 13.2 20235 1 US-07-642-734C-3 34 29 13.2 20235 1 US-07-642-734C-3 35 28.8 13.2 20235 3 US-08-439-009A-3 36 28.8 13.2 777 4 US-09-02-540-3367 37 28.8 13.2 1383 1 US-08-484-044-1 39 28.8 13.2 3183 1 US-08-484-044-1 39 28.8 13.2 3785 1 US-08-252-966B-17 40 28.8 13.2 3785 1 US-08-252-966B-17 41 28.8 13.2 3785 1 US-08-252-966B-17 42 28.8 13.2 17125 4 US-09-92-540-1158 43 28.6 13.1 1140 4 US-09-99-451-116 45 28.6 13.1 1765 4 US-09-799-451-117
	ATCCTAGCACGCTGCCCTGACATCAT 61	TON AND USES THEREOF	Sequence 479, App Sequence 10411, A Sequence 11217, A Sequence 11091, A Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 17, Appli Sequence 11, Appli Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli Sequence 1110, Appli

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US-09-949-016-19194/c
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; ORGANISM: Human
US-09-949-001-36
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19194
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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SEQ ID NO 36
LENGTH: 9174
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Best Local Similarity
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CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
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                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                             Local Similarity
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                                                                       CAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCACCA 198
                                                                                                               CCAGGCCTTCCTGGGGCGCTGTTCCTCCATCCAGCTTAGCCACCTGCCAGGTTAGGCC
                                                                                                                                       CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA 138
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                                     CCCATCCAGAGACATCCACCCGGATCACAGCCCTGCCACCACCACTCCATGCATAGCC
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Pred. No. 0.11;
0; Mismatches
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Pred. No. 8.8e-10;
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                                                                                                                                                                                                                             Length 601;
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                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2153
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US-09-949-016-73784/c
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                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2153
LENGTH: 2393
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6812339
GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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ORGANISM: Human
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les 68; Conserv
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                     16.0%;
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Score 35; DB 4
Pred. No. 0.18;
0; Mismatches
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Pred. No. 0.11;
0; Mismatches
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US-09-949-016-11816/c
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 68
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 2408
                                                                                                                                                                                                                                                                                    Sequence 11816, Application US/09949016 Patent No. 6812339
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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-09-949-016-74
                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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RESULT 9 US-08-304-309-3

Sequence 3, Application US/08304309 Patent No. 5856454 GENERAL INFORMATION:

APPLICANT:

GONZALEZ,

Frank J.

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Ve
; SEQ ID NO 11816
; LENGTH: 7561
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11816
                                                                                                                                                                                                                                                                        ; LENGTH: 7562
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13895
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                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13895
LENGTH: 7562
                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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5230
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                                 CLI
                                                                   CCCATCCAGAGACACCACCCGGATCACAGCCCTGCCACCACCACCACCATGCATAGCC 5231
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Pred. No. 0.28;
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US-08-991-942-3
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                                                                                                                                                 Sequence 3, Application US/08991942
Patent No. 6015673
GENERAL INFORMATION:
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9043
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                  APPLICANT: GONZALEZ, Frank J.

APPLICANT: FERNANDEZ-SALGUERO, Pedro
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRATURE:
NAME/KEY: misc_feature
LOCATION: 1..4447
OTHER INFORMATION: /product= "Pig_DPD"
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                     ADDRESSEE:
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STRANDEDNESS: single
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Steuart Street Tower,
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Townsend and Townsend Khourie and Crew euart Street Tower, One Market Plaza
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Pred. No. 1.9;
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US-09-949-016-11745
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                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                           Sequence 11745, Application US/09949016 Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIO
FILE REFERENCE: CL001307
                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 543-50
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/304
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..4447
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/991,942 FILING DATE:
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California
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88..3162
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Pred. No. 1
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RESULT 13
US-09-774-528-404/c
US-09-774-528-404/c
; Sequence 404, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
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; ORGANISM: Human
US-09-949-016-16163
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SOFTWARE: FastSEQ for Windows Version

SEQ ID NO 11745

; EEQ IT NO 11745

; LENGTH: 36180

TYPE: DNA

ORGANISM: Human

US-09-949-016-11745
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16163
LENGTH: 36181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Patent No. 6812339
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               tch 14.6%; Score 32; 1 al Similarity 53.1%; Pred. No. 5 68; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                            54
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OF DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 11990
LENGTH: 99748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (194
US-09-774-528-404
                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11990
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US-09-949-016-11990/c
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 Query Match
Best Local S
Matches 64
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
FILE REFERENCE: CL001307
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Best Local Similarity 58.5%;
Matches 55; Conservative
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APPLICANT:
APPLICANT:
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TYPE: DNA
ORGANISM: Homo
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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SOFTWARE: pt_FL_genes Version 2.0
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CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
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TITLE OF INVENTION: No. 6743619el Nucleic
TITLE OF INVENTION: Polypeptides
                                                                                                      LENGTH:
TYPE: DI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 TGGCCAGCCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTG
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 64; Conserv
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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   Conservative
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di, Vinod
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                 14.4%;
Score 31.6; Di
Pred. No. 10;
0; Mismatches
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Pred. No. 1.9;
0; Mismatches 39;
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                               DB 4;
   54;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEO ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16518
LENGTH: 99749
TYPE: DNA
ORGANISM: Human
US-09-949-016-16518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-949-016-16518/c
US-09-949-016-16518, Application US/09949016
; Sequence 16518, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
Search completed: September 1, Job time: 73.3315 secs
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                                                                                                                                                                                                   33606 CAGGAAACACTCCCAGGTAGCTGTGTTCTCCAGATGACCATTCACCATGAAAACCG 33549
                                                                                                33606 CAGGAAACACTCCCAGGTAGCTGTCTTCTCCAGATGACCATTCACCATGAAAACCG 33549
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Minimum DB
Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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length: 2000000000
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Match Length
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270
Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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BC013345
AY560836
AX401932
                           AX409747
HUMIGFBP1A
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Compugen Ltd
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                         AX163782 Sequence
L22979 Rat insulin
BC078889 Rattus no
AX095345 Papio anu
G67119 IGFBP1 X1.1
AX409747 Sequence
M74587 Human insul
                                                                                       AL607124 Mouse DNA
BC013345 Mus muscu
AY560836 Spermophi
AX401932 Sequence
AX827271 Sequence
M58634 Rat IGF bin
      M59316 Human insul
                                                                                                                                                                                     Description
                                                                                                                                                 AC136382 Rattus no
X67493 M.musculus
                774587 Human insul
G19994 sWSS752 Eri
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45	44	C 43	42	41	40	39			c 36			33	32	31	30	29	28	27	26	25	24		c 22		20
35	35.6	36.6	36.6	36.6	36.6	36.8	36.8	36.8	37.8	37.8	37.8	43.2	43.2	44.4	49	50.4	51	51	51	51	51	59.2	59.2	59.2	60.8
13.0	13.2	13.6	13.6	13.6	13.6	13.6	13.6	13.6	14.0	14.0	14.0	16.0	16.0	16.4	18.1	18.7	18.9	18.9	18.9	18.9	18.9	21.9	21.9	21.9	22.5
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BV184757 sqnm14591	AE016922 Chromobac	AL713999 Human DNA	AY316591 Homo sapi	U47654 Homo gapien	Z18922 H.sapiens D	BX640447 Bordetell	BX640427 Bordetell	BX640428 Bordetell	AX348680 Sequence	AX345899 Sequence	AX251887 Sequence	AC097039 Rattus no	M17088 Rat pyruvat	M89791 Rattus norv	G67173 IGFBP1 5'A	M23592 Human insul	X05684 Rat L-PK ge	AX827302 Sequence	E14395 gDNA encodi	AR175909 Sequence	A57715 Sequence 1	AC148834 Pan trogl	AC146117 Pan trogl	AC146152 Pan trogl	AC091524 Homo sapi

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                                                                                                                                                                                                                                                                                                                                              Unterman,T.G., Lacson,R.G., McGary,E., Whalen,C. and Goswami,R. Biochem. Biophys. Res. Commun. (1991) In press Original source text: Rattus norvegicus (strain Sprague-Dawley) male adult liver DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATILGFZ 1181 bg
Rattus norvegicus insulin-like
M84484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          insulin-like growth factor.
Rattus norvegicus (Norway rat)
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                                                                                                                                                      Conservative
                                                                                                                                                                                                                   /sex="male"
/tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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99.5%;
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                                                                        Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Sonegl, X., So., Sovetle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tringey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Warren, J., Waite, F., Williams, G., Wilson, R., Wleczyk, R., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wleczyk, R., Woden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., hiver, C., White, H., C., Weinstock, G. and Gibbs, R.A.
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AC136382.1 GI:24462257
HTG; HTGS_PHASE1.
Rattus norvegicus (Norway rat)
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                       (bases 1 to 185148)
Genome Sequencing Consortium
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid,
Chemistry: Dye-terminator Big Dye: 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 135613 bases at least Q40
Consensus quality: 140849 bases at least Q30
Consensus quality: 145680 bases at least Q20
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Center clone name: CH230-97018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
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                                      TCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCA
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                                                                                                                    42383; gap of unknown 143821; gap of unknown 144538; contig of 1338 by 43821; gap of unknown 146538; contig of 1983 by 448721; gap of unknown 14538; contig of 1983 by 50002; contig of 1983 by 50002; contig of 2054 by 50004; gap of unknown 145394; contig of 2654 by 50004; gap of unknown 145394; contig of 2654 by 50004; gap of unknown 145394; contig of 1983 by 61132; gap of unknown 145394; contig of 3003 by 61232; contig of 4072 by 61232; conti
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2 (bases 1 to 1363)

Mohn,K.L., Waddle,J.R. and Taub,R.

Comparison of mouse and human IGFBP-1 genes reveals

Comparison of mouse sequence and conservation of all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1992) R.A. Taub, Univ. of Pennsylvania, Howard Hughes Medical Institute, Clinical Research Bldg., Room 475, 422 Curie Boulevard, Philadelphia, PA 19104-6145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mohn,K.L., Bucan,M. and Taub,R. Structure and localization of the IGFBP-1 gene and its expression during liver regeneration Hepatology 19 (3), 656-665 (1994) 94164648
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insulin-like growth factor
Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1363)
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3 (bases 1 to 1363)
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764. .768
792. .1336
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/cell_type="fibroblast"
/clone_lib="genomic, lamb/dev_stage="embryo"
con__soa_
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/codon_start=1
/product="insulin-like growth factor
/protein_id="CAN47832.1"
/db_xref="GOA:P47876"
/db_xref="GOA:P47876"
                                                                                             /note="mRNA
964. .>1336
                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="JW2.1"
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                                                                                                             site"
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Best Local
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                                                                                   source
                                                                                                                                                                                                                                                                     AL Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
    champridgeshire, CB10 1SA, UK. E-mail enquiries:
    humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
    On Apr 12, 2002 this sequence version replaced gi:1947866.
    During sequence assembly data is compared from overlapping clones.
    Where differences are found these are annotated as variations
    together with a note of the overlapping clone name. Note that the
    variation annotation may not be found in the sequence submission
    corresponding to the overlapping clone, as we submit sequences with
    only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
    regions were either double-stranded or sequenced with an alternate
    chemistry or covered by high quality data (i.e., phred quality >=
    30), an attempt was made to resolve all sequencing problems, such
    as compressions and repeats; all regions were covered by at least
    one plasmid subclone or more than one MI3 subclone; and the
    assembly was confirmed by restriction digest. The following
    abbreviations are used to associate primary accession numbers given
    in the feature table with their source databases: Em., EMBL; Sw.,
    SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         857
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                                                                                                                                                       constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse DNA sequence from clone
                                                                                                                                                                                                                                                          database can be found at
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                               pBACe3.6.
/organism="Mus musculus'
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
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                                                                                                     ocation/Qualifiers
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Pred. No. 4.3e-45;
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BC013345
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                                                                                                                                                                                                                                                                                                                                                     Strauberg, R.U., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsleh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyukl, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Kodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                              Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC013345

1569 bp mRNA linear ROD 30-JUN-Mus musculus insulin-like growth factor binding protein 1, mRNA (cDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                                                                                                                                                                                                       Strausberg, R.
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Mammalia; Eutheria; Rodentia;
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/clone_lib="RPCI-23"
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Pred. No. 4.3e-45;
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                                                                                                                                 nci.nih
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AY560836
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Li,Y., Klimanis,D. and Hallenbeck,J.M. Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: i Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                          Spermophilus tridecemlineatus (thirteen-lined ground squirrel) Spermophilus tridecemlineatus
                                                                                                                                                                                    AY560836.1 GI:45505308
                                                                                                                                                                                                                                     Spermophilus tridecemlineatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Rahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                         AY560836
                                                                          Spermophilus
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                                                                                                                                                                                                                                                                                                                                                                   CACACGGCCATCTGCCCAGAGAGAGCTGTGACCACCACCACCTTCCGCTACCTAGCTA 265
                                                                                                                                                                                                                                                                                                                                               CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCCAGCCAGGATGGTCCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                    1 (IGFBP1) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="insulin-like growth factor binding protein 1"
/protein_id="AAH13345.1"
/db_xref="GI:15426483"
/db_xref="HOCUSID:16006"
/db_xref="MGI:96436"
/translation="MPEFLTVUSWPFLILLSFQIGVAAGAPQPWHCAPCTAERLGLCP
PVPASCPEISRPAGGGCTPCALPMGAAGGVATARCAQGLSCRALPGEPRPLHALTRG
GGACVPEPAAPATSTLSSSQHEEAKAAVVSADELSESPEMTEEGLLDSFHLMAPSRED
QDILWANAISTYSSMRAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
QDILWANAISTYSSMRAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
/db_xref="MGI:96436"
204. .1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVHN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Igfbp1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Liver, normal./clone_lib="NCI_CGAP_Li9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="FVB/N"
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/clone="MGC:14075 IMAGE:4161889"
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Pred. No. 3.2e-18;
                                                                                                                                                                                                                                                  1507 bp
                                                                                                                                                                                                                  1507 bp mRNA eatus insulin-like complete cds.
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                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Sciuridae; Sciurinae;
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Matches 144;
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Best Local Similarity
                                                                                                                                                                                                                                                      Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                          Mendrick, D.,
Elashoff, M.R.
                                                                                                                                                                                                                                                                                                                                                                         Sequence 1608 from Patent W00210453 AX401932
                                                                                                                     Gene Logic,
                                                                                                                                         Patent:
                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-FEB-2004) StrokeBranch, NINDS/NIH, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li,Y., Klimanis,D
Direct Submission
                                                                                                                                                          Molecular toxicology
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                                                                                                                                                                                                                                                                                                                                                                                                                AX401932
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Y., Klimanis,D. and Hallenbeck,J.M
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                                                                                                                                     WO 0210453-A
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PVPSSCPELSRPAGCGCCPMCALPLGAACGVATARYARGLSCRALPGEPRPLHALTRG 
QGACVPEPATPTASGLSS IEKEEAKASMVPERVPPESAEMTERQLLES FHLMASSSED 
QPILWMAISTYKSMRAREMADIKKWKQPCRRELYKVLERLAKAQQKAGEBIYKFVLPN 
CNKNGFYHSKQCETSLDGEAELCWCVYPWSGRRIPGSLEIRGDPNCHQYFNVQN"
                  organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                            Location/Qualifiers
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/protein_id="AAS67029.1
/db_xref="GI:45505309"
note="EMBL/GenBank Accession No. NM_013144"
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1608 07-FEB-2002;
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Pred. No. 8.8e-12;
0; Mismatches 54
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COMMENT
FEATURES
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RATIGEB
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ACCESSION
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Best Local S
Matches 77
                                                                 JOURNAL
MEDLINE
                                                                                                        AUTHORS
TITLE
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Best Local Similarity
Matches 77; Conserv
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JOURNAL
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                                                                         1 (bases 1 to 1500)
Mohn, K.L., Melby, A.B., Tewari, D.S., Laz, T.M. and Taub, R. The gene encoding rat insulinlike growth factor-binding is rapidly and highly induced in regenerating liver Mol. Cell. Biol. 11 (3), 1393-1401 (1991)
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IGF binding protein-1.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                       Original
                                                                   91141487
                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boess, F., Suter-Dick, L. and Wolf, D. Methods for the toxicity prediction Patent: EP 134484-A 5 17-SEP-2003, F. HOFFMANN-LA ROCHE AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata,
Mammalia, Eutheria; Rodentia;
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Sequence 5 from Patent EP1344834.
AX827271 GI:39837360
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              source text: Rat, cl
Location/Qualifiers
1. .1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
/organism="Rattus norvegicus"
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98.7%;
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Pred. No. le-11;
0; Mismatches 1;
                                    cDNA to mRNA.
                                                                                                                                                           Craniata; Vertebrata;
Sciurognathi; Muridae;
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Sciurognathi;
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thi; Muridae;
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Murinae;
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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AX163782
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Matches 77
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61
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AX163782
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                                                                                       77;
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77; Conserv
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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CACTTCCGCTACTATCTA 78
                                          CACTTCCGCTACTAGCTA 265
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                                                                                        Conservative
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46 from Patent WO0138579.
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/db_xref="taxon:10116"
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/tissue_type="regenerating
/dev_stage="adult"
160 _ .978
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/product="IGF binding
/protein_id="AAA41380.
/db_xref="GI:204733"
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/strain="Fisher"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="IGF binding protein-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.3%;
98.7%;
                                                                                                                                                                                .5001
                                                                                                 28.3%;
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                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    85
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                                                                                      Score 76.4; DB 6;
Pred. No. 1e-11;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76.4; DB 10;
Pred. No. 1e-11;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                     rat)
                                                                                                                                                                                                                                    o,V.A., Ramseh,T.M. and Gerwein,R.W. agents using nsaid-induced differential
                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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).1"
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RESULT 11 RATIGFBA

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                    188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Nov 30, 1995 this sequence version replaced gi:385167. Original source text: Rattus norvegicus (strain Sprague-Dawley)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L22979.1 GI:1098472
insulin-like growth factor binding
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94250701
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat insulin-like
                                                                Similarity
CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCCTGTGACCAC
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QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="IGFBP-1"
join(153. .525,1850.
/gene="IGFBP-1"
                                                                                                                                                                                                         3003.
                                                                                                                                                                                                                                                                                                                                                                                                        CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="insulin-like growth factor binding protein"
/protein_id="AAA82581.1"
/db xref="Gi:1098473"
/translation="MPEFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP
                                                                                                                                                                       number=3
                                                                                                                                                                                     3003. .4089
/gene="IGFBP-1"
                                                                                                                                                                                                                    number=3
                                                                                                                                                                                                                                  'gene="IGFBP-1"
                                                                                                                                                                                                                                                                                /gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                              1850. .2034
/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="liver"
/dev_stage="adult"
                                                                                                                                            number=4
                                                                                                                                                                                                                                                                   number=2
                                                                                                                                                                                                                                                                                                                number=2
                                                                                                                                                                                                                                                                                                                                                             number=1
                                                                                                                                                                                                                                                                                                                                                                             'gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
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                                                             28.3%;
98.7%;
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                                                                                                                                                          .4743
                                                                                                                                                                                                                                                                                                .2873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lib="Clontech EMBL-3 SP6/T7"
                                                           Score 76.4; DB 10;
Pred. No. 1e-11;
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                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .3002,4090.
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; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROD 30-NOV-1995
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
RS trausberg, R.L., Feingold, E.A., Grouse, L.H., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: e Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 6981079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help dek
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Director MGC Project.

Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) National Institutes Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus insulin-like growth factor binding protein 1, mRNA (cDNA clone MGC:93595 IMAGE:7129185), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.
Dickson, M., Schmutz, J., Grimwood, J., Rodri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                  Direct Submission
Submitted (11-APR-2002) Department of Obstetrics and Gynecology, Submitted (11-APR-2002) Department of Submitted (11-APR-2002) Department of Obstetrics and Gynecology, Submitted (11-APR-2002) Department of Obstetrics (11-APR-2002) Dep
                                                                                                                                                                                                                                                                                                                                                                                                                           Kim,J.J., Taylor,H.S., Akbas,G.E., Foucher,I., Trembleau,A., Jaffe,R.C., Fazleabas,A.T. and Unterman,T.G. Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells Biol. Reprod. 68 (1), 24-30 (2003)
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                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 3886)
Kim, J.J., Jaffe, R.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Papio anubis
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PVPASCPALSRAGCGCCPTCALFLGARACGVATARCAQCISCRADGEPRELHALTRG
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QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTERGLLDSFHLMAPSFEB
QPILWNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
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/protein id="AAH78889.1"
/db_xref="GI:50927647"
/db_xref="LocusID:25685"
/db_xref="RATMAP:44422"
/db_xref="RGD:2872"
                                                       /organism="Papio anubis"
/mol_type="genomic DNA"
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/gene="IGFBP-1"
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/clone_lib="NIH_MGC_236"
/lab_host="DH10B"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 448)
Cox,D.G., Boillot,C. and Canzian,F.
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                                                                                                                                                                                                                                                                                     Tel: +33-4-72738698
                                                                                                                                                                                                                                                                                                                                              Contact: Federico Canzian
                                                                                                                                                                                                                       Primer B:
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3655. .>3886
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/translation="MSEVPVARVWLVLLLLLTVQVGVTASAPWQCAPCSAEKLALCPPV
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                                                                                                                                                                                                                                                                                                                                                                                            Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G. Gene expression profiles in liver cancer Patent: WO 0229103-A 2394 11-APR-2002; GENE LOGIC INC (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX409747 6128 bp D
Sequence 2394 from Patent WO0229103.
AX409747 GI:21442452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                  CAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                    TAACCC-----GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC 162
CCATCTGCCCAGAGAGCTGTGACCACCACTTC 253
                             GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCGCGCCCC
                                                                                          TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
                                                                                                                                                     CACTAGCAAAACAAACTTATTTTGAACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACCCTCCCAGAGAGCACTGGCCACCGCTCC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="genomic DNA"
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/clone lib="Human"
1. .448
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/note="EMBL/GenBank Accession No. M74587"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                  Score 60.8; DB 6;
Pred. No. 4.5e-07;
0; Mismatches 52
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645 CCACCCTCCCAGAGAGCACTGGCCACCGCTCC 676

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Search completed: September 1, 2005, 03:26:49 Job time : 1685:14 secs

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Perfect score:
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Copyright (c) 1993 - 2005
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W30013
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AI1985039
CO573026
CV127049
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CA478518
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AI196314
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                        BY771317 BY771317
A1785818 ui78h05.y
A1196314 ui79h07.y
A1530146 ui89f09.y
A1530146 ui89f09.y
A1530313 ui91f01.y
A152939 ui87c09.y
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     W30013 mc24c07.rl
BB660958 BB660958
CD561711 B0435D02-
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13.0	13.0	13.0	13.0	13.0	13.0	13.6		13.6	13.8	14.4	15.9	21.9	22.5	22.5	22.8	22.9	23.3	23.9	24.2	25.0
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BM772026	BG388790	BG283072	AA443181	BX282084	T87256	CNS007WH	CNS02Q6E	BF829782	AW655007	BU684425	AZ840793	AA060360	CR595377	CR621807	AW916227	BB604790	AA105355	CK473709	CK472246	AA674302
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K-EST0056	602414492	602406695	zx98h10.r	BX282084	87256 yd91c06.rl	Drosophil	Tetraodon	MR3-HN006	105551 MA	UI-CF-ENO	2M0138D02	mj67a12.r	full-leng	full-leng	EST347531	BB604790	mp37d09.r	AGENCOURT	AGENCOURT	vp96g10.r

ALIGNMENTS

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REFERENCE
AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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JOURNAL
Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9443 row: j column: 02
High quality sequence stop: 581.
Location/Qualifiers
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602026605F1 NCI_CGAP_Li9 MuB
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF236974.1 GI:11150891
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  Conservative
                                                                                                /db_xref="taxon:10090"
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/clone_lib="NCICGAP_Li9"
/clone_lib="NCICGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                         organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                         . .1013
                     36.4%;
Score 98.2; DB 2;
Pred. No. 1.5e-18;
0; Mismatches 8;
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155 TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACACAACCCCAGCGAGCATTGAACACTG

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                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY783538 RIKEN full-length enriched, 17.5 days embryo Mus musculus cDNA clone L930176D05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 310)
Carninci, P., Waki, K., Shiraki, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                              Similarity
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TGCCCAGAGAGCTGTGACCACCACTTCCGCTACCTAGCTA 265
                                                                                                ATGGTCCACTGCCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 119
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                                                                     ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (house
                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   visit our web site (http://genome.gsc.riken.jp/) for
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/dev stage="17.5 days embryo"
/clome lib="RIKEN full-length enriched, 17.5 days embryo
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                                                                                                                                                       0;
                                                                                                                                                                            Score 87.8; DB 6;
Pred. No. 1.6e-15;
                                                                                                                                                          Mismatches
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d, 17.5 days embryo whole body
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E 1 (bases 1 to 331)

S Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y., Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6B), 1273-1289 (2003)
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The Institute of Physical and Chemical Research (RIKEN)
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Mus musculus (house mouse)
Mus musculus
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Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
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Please visit our web site (http://genome.gsc.riken.jp/)
TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC 61
                                                                                                                                        ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
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RIKEN full-length enriched, 17.5 days embryo
ulus cDNA clone L930292H24 5', mRNA sequence.
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/mol_type="mRNA"
/strain="C57BL/6J"
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0; Mismatches 7;
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Scarninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saico, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikiwa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinia, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.

Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia

Genome Res. 13 (6B), 1273-1289 (2003)
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401 bp mRNA linear EST 02.
ui78h05.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
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Please visit our web
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mus musculus (house mouse)
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BY771317 RIKEN full-length enriched, 17.5 days embryo whole musculus cDNA clone L930052G15 5', mRNA sequence.
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/clone="L930052G15"
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AII96314
480 bp mRNA linest ui71a07, yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1887828 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus factor binding (MOUSE);, mRNA
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Other ESTS: u178h05.xl
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 401)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                                                                                                           TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Sugano mouse liver mlia"
/note="Forgan: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the DME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing; 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'clone="IMAGE:1888569"
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92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.8; DB 1;
Pred. No. 3.4e-15;
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                                                                                                                                                     RESULT 7
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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AI530146
706 bp mRNA linear EST 18-MAR-19 u189f09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULI-LIXE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 480)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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AI196314.1 GI:3748920
EST.
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                            GCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                  TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII
(CACTGTGTGT); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shou
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
Constructed by Dr. Surio Scoren (Intercett).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 86.8; DB 1;
Pred. No. 3.6e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 480;
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RESULT 8
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AI530146
AI530146.1
                 AIO98594 Tinear EST 20-ue31e07.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
AI098594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pMEISS-FI3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG]; digested
and cloned into distinct DraIII sites of the pMEISS-FI3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shou
be used to isolate the cDNA insert. Size selection was
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| db_host="DH10B"
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mol_type="mRNA"

strain="C57BL"
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92.9%;
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Pred. No. 3.9e-15;
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 706;
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RESULT 9
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Best Local
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                                                                                                                                                                                                                                                                            228
                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                   A1530313 785 bp mRNA linear EST 18-MAR-1999 u191f01.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889785 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN I PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubud Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
ведиепсе
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:930344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                       GCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                          TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
                                                                                                                                                                                                                                                                                                                                                      TGGTCCACTGCCCGACGACACACACACCCAGCGAGCATTGAACACTGCACACGGCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Sugano mouse liver mlia"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pMEL8S-FL3; Site_1: DraIII
(CACCATGTGT); Site_2: DraIII (CACCATGTG); lst Etrand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG]; digested
and cloned into distinct DraIII sites of the pMEL8S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/db_xref="taxon:10090"
/clone="IMAGE:1481988"
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/lab_host="DH10B"
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RESULT 10
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AI530313.1
EST.
A1529939
799 bp mRNA linear EST 18-MAR-11 ui87c09.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889392 5' similar to gb:M59316 Tnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                                                                                                                                                                                                               GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Nigano mouse liver mlia"
//clone_lib="Nigano mouse liver mlia"
//clone_lib="Crgan: liver; Vector: pME188-FL3; Site_1: DraIII
(CACTGTGTGT6); Site_2: DraIII (CACCATGT6); lst Strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTG6], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGT6, 3' site CACCATGT6). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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Pred. No. 4e-15;
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ACCESSION
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Best Local Similarity
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  CA478518
CA478518.1
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AGENCOURT 10789306 NIH MGC 152 MUS
IMAGE:6766752 5', mRNA sequence.
CA478518
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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AI529939.1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                     GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
                                                                                                                                                                                                                                                                                                                    TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(AACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). KhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). CAUSTOM primers GTGCTGCAGCTCGAGCACA."
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/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1889392"
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/lab_host="DH10B"
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               Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,F. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R. Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                   uk28b10.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1970299 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Mark Bittinger
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLKM00138 row: m column: 23
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Unpublished (1999)
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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EST.
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Tissue Procurement: Bradfield Laboratory
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/db_xref="taxon:10090"
/clone="IMAGE:6766752"
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Pred. No. 4e-15;
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Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (house mouse)
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                              Waterston, R
                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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The WashU-HHMI Mouse EST Project
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//clone_Torgan: liver; Vector: pMELBS-FL3; Site 1: DraIII
(CACCTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMELBS-FL3
vector (5' site CACCTGTGTG, 3' site CACCATGTGT). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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|lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:1890210"
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92.9%;
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Pred. No. 4e-15;
D; Mismatches
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                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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REFERENCE
AUTHORS
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VERSION
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AI785039
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Best Local :
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 380)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                   ui73a06.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888018 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                         AI785039
AI785039.1 GI:5332755
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: custom primer used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 265
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                                                                                                                                                                                                                                                                        musculus (house mouse)
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Location/Qualifiers
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//clone="Corgan: liver; Vector: pMELBS-FL3; Site_1: DralII
//note="Organ: liver; Vector: pMELBS-FL3; Site_1: DralII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DralII adaptor [TGTTGGCCTACTGTG], digested
and cloned into distinct DralII sites of the pMELBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
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/strain="C57BL"
/db_xref="taxon:10090"
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Pred. No. 1.1e-14;
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Search completed: September Job time: 2054.88 secs

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_ESTs: ui73a06.x1
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                                                                                                                                          TCCACTGCCCGACGACACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCC 230
CAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                 /Clone_lib="Sugano mouse liver mlia"
//Clone_lib="Sugano mouse liver mlia"
//CACTGTGTGT; Site 2. DraIII (CACCATGTG); lst Etrand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTGATGTG], digested
and cloned into distinct DraIII sites of the pME188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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strain="C57BL"
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'clone="IMAGE:1888018"
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                                                                                                                                                                                                                                               30.4%;
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                                                                                                                                                                                                                                               Score 82.2; DB 1;
Pred. No. 8.3e-14;
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Maximum Match 100%
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    270
270
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l: /cgn2_6/ptodata/2/pubpna/US07_
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:/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USO9E_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USOP_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USOP_PUB.seq:*
:/cgn2_6/ptodata/2/pubpna/USOP_PUBCOMB.seq:*
:/cgn2_6/ptodata/2/pubpna/USOP_PUBCOMB.seq:*
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                    US-09-972-916A-3

US-09-972-916A-6

US-09-972-916A-4

US-09-972-916A-5

US-09-972-916A-2

US-09-917-800A-1608
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                    Sequence 3, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 1608, Ap
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Sequence 5, Appl:
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US-10-363-	US-10-087-192-	US-10-282-122A-332	US-10-425-115-	US-10-367-094-	US-09-764-872-	US-10-072-012-2	US-10-120-988-	US-10-292-798-	US-10-017-161-201	US-	US-10-322-281-	US-10-437-963-7918	US-10-437	US-10-108-260A-223	US-10-250-615-	US-10-741-600-	US-10-741-601-	US-10-011-585/	US-10-027-632-16433	US-10-027-632-16433	US-10-739-930-5461	US-10-027-632-174961	US-10-027-632-17496	US-10-085-117-172	US-10-221-613-148	US-10-311-455-970	US-10-152-319A-2150	US-10-388-934-36	US-09-972-916A-	US-09-972-916A-	US-09-972-91	US-10-893-3	US-10-893-	US-10-756-1	US-09-880-107-2393	US-10-152-319A-	US-10-191-803-7
e 40493,	Φ	e 33251	2833	equence 169,		equence 29,	404,	1663	2017	Sequence 31, Appl	492	791	.,	223	33,	179	Sequence 5746, Ap		Sequence 164336,		equence	Ð	ö					æ	ഗ	4.	_	_	e 1	ce 1484,	2393,	e 1613	equence 73, Ap

ALIGNMENTS

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US-09-972-916A-3
; Sequence 3, Application US/09972916A
; Patent No. US20020107198A1
; GENERAL INFORMATION:
; APPLICANT: Thule, Peter M.
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                                                                                                                                                                                                          OTHER INFORMATION: Synthesized US-09-972-916A-3
                                                                                                                        Query Match
Best Local S
Matches 270
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CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION FILE REFERENCE: US 1292/01 (VA)
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                        / Match 100.0%;
Local Similarity 100.0%;
nes 270; Conservative 0
  61 AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT 120
                                                                    1 CATGGGCGCACGGGGCACTCCCGTGGTTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA
                                      CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTATCACAAGCA 60
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Pred. No. 3.2e-86;
); Mismatches 0;
                                                                                                                                                                 Length 270;
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Sequence 6, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
LENGTH: 423
TYDE: NNA
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US-09-972-916A-4
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US-09-972-916A-6
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                                                                                    Sequence 4, Application US/09972916A Patent No. US20020107198A1 GENERAL INFORMATION:
          APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10
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Best Local Similarity
PRIOR APPLICATION NUMBER: US 60/239,113
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ORGANISM: Artificial Sequence
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Sequence 5, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INS
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
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US-09-972-916A-5
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NUMBER OF SEQ ID NOS: 6
SEQ ID NO 4
                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 220; Conserv
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Best Local Similarity
Matches 220; Conserv
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ORGANISM: Artificial Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Synthesized
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                        CCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 270
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Pred. No. 4.7e-68;
0; Mismatches 1
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APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
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PRIOR APPLICATION NUMBER: US 60/22,040
PRIOR FILLING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/22,880
PRIOR FILLING DATE: 2000-011-02
PRIOR PELLONG DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILLING DATE: 2001-05-11
PRIOR PELLONG DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,798
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
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SEQ ID NO 2
LENGTH: 219
TYPE: DNA
ORGANISM: Rattus norvegicus
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PATENT NO. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT APPLICATION NUMBER: US/09/972,916A
PRIOR APPLICATION NUMBER: US/09/972,916A
PRIOR APPLICATION NUMBER: US/09/972,916A
PRIOR FILING DATE: 2000-10-11
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Best Local :
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FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOPTWARE: Patentin version 3.1
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US-10-191-803-73
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; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013144
US-09-917-800A-1608
                                                                                                                                      Sequence 73, Application US/10191803 Publication No. US20040014040A1 GENERAL INFORMATION:
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Publication No. US20040005547A1
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Best Local
APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
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ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                          248 CACTTCCGCTACTAGCTA 265
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98.7%;
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Pred. No. 1.5e-16;
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                                                                                 PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILLING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILLING DATE: 2001-07-10
PRIOR PILLING DATE: 2001-07-10
PRIOR PPLICATION NUMBER: US 60/315,047
PRIOR PPLICATION NUMBER: US 60/324,928
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILLING DATE: 2001-10-22
PRIOR FILLING DATE: 2001-10-22
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR PPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR PILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
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GENERAL INFORMATION
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SEQ ID NO 73
LENGTH: 1500
SEQ ID
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TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR PILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
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                                           Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 2221
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                        PatentIn Ver.
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Higgs, Brandon
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Pred. No. 1.5e
0; Mismatches
                                                                 See File Wrapper or PALM
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US-09-880-107-2393
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US-09-880-107-2393
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SEQ ID NO 2393
LENGTH: 6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Horne, I
APPLICANT: Vockley
APPLICANT: Scherf,
APPLICANT: Gene Lo
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                             Query Match
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. NM_013144
                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
645
                                                                   473 CACTAGCAAAACTTATTTTGAACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCAT 532
                                                                                                  163 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                                                                       113 TAACCC-----
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                                                                                                                                                                                                                                                                             141;
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                   CCATCTGCCCAGAGAGCTGTGACCACCACTTC
                                                                                                                                    TAACCTCCTGGTGCAAGTGGCGGCCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGC
CCACCCTCCCAGAGAGCACTGGCCACCGCTCC
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Scherf, Uwe
                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                           22.5%;
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98.7%;
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                                                                                                                                                                     - GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC 162
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Pred. No. 8.9e-11;
0; Mismatches 52;
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Pred. No. 1.5e-16;
); Mismatches 1
676
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                                                                                                                                                                                                                                                                                                           Length 6128;
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RESULT 11 US-10-756-149-1484

Sequence 1484, Application US/10756149 Publication No. US20050181375A1 GENERAL INFORMATION:

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; ORGANISM: Human
US-10-893-315-126
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US-10-893-315-126
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; ORGANISM: Homo Sapiens
US-10-756-149-1484
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Publication No. US20050147987A1

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION ITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.9
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: FastSEQ for Windows Version SEQ ID NO 126 LENGTH: 9173
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Best Local Similarity 66.5%;
Matches 141; Conservative
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CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1484
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TITLE OF INVENTION: MOTHL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aziz, Natasha APPLICANT: Zlotnik, Alb
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                                                               CAGCATGGTCCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTGC-ACACGG
                                                                                                                                         TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGC
                                                                                                                                                                                     TAACCC------GTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGC 162
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Pred. No. 8.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60.8; DB 22; Pred. No. 1e-10; 0; Mismatches 52;
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-CATCCAGCGAGCATCTGCCGCCGCGCCGCCG
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; Sequence 1, Application US/09972916A

PAtent No. US20020107198A1

; GENERAL INFORMATION:
; APPLICANT: Thule, Peter M.
; TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INS FILE REFERENCE: US 1292/01 (VA)
; CURRENT APPLICATION UNMBER: US/09/972,916A
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/239,113
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 9174
; TYPE: DNA
; ORGANISM: Human
US-10-893-315-160
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US-09-972-916A-1
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Publication No. US20050147987A1
GENERAL INFORMATION:
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                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Matches
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2172
NUMBER OF SEQ ID NOS: 2172
                                                                                                       TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                     FEATURE:
                                                                                                                                                            LENGTH: 51
Local Similarity
nes 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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Conservative
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              18.9%; Score 51; DB 9; L
100.0%; Pred. No. 6.4e-08;
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Mismatches
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                                   Length 51;
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Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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270
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     1202784 seqs, 818138359 residues
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Copyright (c) 1993 - 2005
     , Gapext 1.0
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              US-09-949-001-30
US-08-945-140-1
US-08-945-140-1
US-08-949-016-11786
US-09-949-016-119194
US-09-949-016-73784
US-09-949-016-7153
US-09-949-016-11816
US-09-949-016-11816
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Sequence 30, Appl Sequence 1, Appli Sequence 1, Appli Sequence 11786, A Sequence 11786, A Sequence 17205, A Sequence 2153, Appli Sequence 2153, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11745, A Sequence 11745, A Sequence 11745, A Sequence 11745, A Sequence 16153, Appli Sequence 16154, A Sequence 16518, A Sequence 16590, A Sequence 16590, A Sequence 16992, Sequence 16992, Sequence 16992, Sequence 11990, A Sequence 11993, Sequence 1341, Ap Sequence 1341, Ap Sequence 1381, Ap Sequence 1381, Ap Sequence 1381, Ap Sequence 1381, Ap Sequence 1389, Ap
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Q	RESULT 1 US-09-949-001 Sequence 30 Patcent NO. GENERAL INF APPLICANT: ITTLE OF I ITILE OF I ITILE REFER CURRENT AP CURRENT AP CURRENT APIL PRIOR FILI PRIOR FILI NUMBER OF SOFTWARE: SOFTWARE: SEQ ID NO 3 LENGTH: 90 TYPE: DNA ORGANISM: US-09-949-001 Query Match Best Local Matches 14	00 0 00 0000 444444008 544321
113 TAACC 113 TAACC 113 TAACC 113 TAACC 1163 CAGCA 1197 GAGCA 222 CCATC		00000000000000000000000000000000000000
TAACCC TAACCC TAACCTCTG TAACCTCTG CAGCATGGTC		111.3 111.3 111.0 111.0 10.9 10.8 110.7 110.7 110.7 110.7 110.7 110.7 110.7 110.7 110.7 110.7 110.7 110.7
GCAAAACAAACTTATT GCAAAACAAACTTATT GCAAAACAAACTTATT GCCTGGTGCAAGTGGC TGGTCCACTGCCCACCCACCCACCCACCCACCCCAC	30 Application US/09949001 682536 ORMATION: VENTER, J. Craig et al. NVENTION: POLYMORPHISMS I NVENTION: POLYMORPHISMS I NVENTION: WITH OSTEOPORO ENCE: CL000789 PLICATION NUMBER: US/09/9 PLICATION NUMBER: 60/231,32 PROBLE: 2000-09-08 SEQ ID NOS: 848 FastSEQ for Windows Versi 0 1,73 Human -30 22.5%; Scor Similarity 66.5%; Pred 1; Conservative 0; M	28497 4 40181 4 40183 4 1056 3 21956 4 488 4 11101 4 2205 4 2205 4 4348 4 1348 5 1383 1 1383 1
CARCHOCHANNIC IN I I I I I I I I I I I I I I I I	01 N IN ROSI ROSI 323 323 323 sion	US-09-902-540-48 US-09-902-540-17 US-09-949-016-17 US-09-902-540-12 US-09-902-540-12 US-09-902-540-12 US-09-205-258-11 US-09-205-258-11 US-09-205-258-11 US-09-252-991A-1 US-09-252-991A-1 US-09-252-991A-1 US-09-49-016-155
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TTC 253	OP DETECTION AND	Sequence
	USES THEREOF	14899, Ap 17016, Ap 17016, Ap 1, Appli 2783, Ap 2783, App 1119, App 10411, App 11217, A 112217, A 11

RESULT 2
US-09-949-001-36
(S-09-949-001-36
; Sequence 36, Application US/09949001
; Patent No. 6825336
; Patent No. 6825336
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: VENTURER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF

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PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 9174
Type: No. 2007-11-15
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; ORGANISM: Human
US-09-949-001-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Applic
Patent No. 6309878
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Best Local Similarity
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CURRENT FILING DATE: 2003-01-15
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                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/04558
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96,
FILING DATE: 12-APR-1996
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,140
NAME: SAVITZKY ESQ., MAXTIN F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: EX95002-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR VECTOR 10
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APPLICANT: KAHN, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
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ZIP: 19426
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 500 Arcola Road, Mailstop 3C43 CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Pred. No. 3.7e-10;
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RESULT 4
US-08-791-849A-14
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 base pairs
; TYPE: nucleic acid
TYPE: nucleic scid
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GENERAL INFORMATION:
APPLICANT: Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 13011 base pairs
TYPE: nucleic acid
                                                                   ORGANISM:
FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordporfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Method for Increasing Stora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
                                    FEATURE
                                                                                                                                                         ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                   TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 805 Fifte
CITY: Washington
STATE: D.C.
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Local Similarity 100.0%; F
hes 51; Conservative 0;
                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/791,849A FILING DATE: January 30, 1997
                     NAME/KEY:
                                                      LOCATION:
                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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805 Fifteenth Street, N.W., #700
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VENTION: Method for Increasing Storage
                                                  join(3212..3218, 3766..3948, 5917..6008, 6152..6283, 6418..6604, 6921..7191, 7302 9298..9479, 10163..10269)
exon
join(3194..3218, 3766..3948, 5917..6008.
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                                                                                                                                         rat (Rattus norvegicus)
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Pred. No.
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                                                                    7302..7452, 7665..7817, 7911..8077
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US-09-949-016-11786
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                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 681233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11786
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17205
LENGTH: 15108
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Patent No. 6812339
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Best Local S
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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LOCATION:
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ilarity 90.7%;
Conservative
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6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910,
9480..10162)
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Pred. No.
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OF DETECTION
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US-09-949-016-73784/c
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US-09-949-016-17205
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                PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
PILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                       Sequence 73784, Appatent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows
SEQ ID NO 19194
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Best Local Similarity
Matches 39; Conser
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GENERAL INFORMATION:
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TITLE OF INVENTION: POLYMORRHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FALLIGATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR PRIOR PAPELICATION NUMBER: 60/241.756
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PELICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
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for Windows Version
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55.3%;
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Indels

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SEQ ID NO 73784

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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-73784
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US-09-949-016-2153/c
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Sequence 74, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2153
LENGTH: 2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Patent No. 6812339
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Pred. No. 0.14;
0; Mismatches
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Pred. No.
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OF DETECTION AND USES THEREOF
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; ORGANISM: Human
US-09-949-016-11816
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US-09-949-016-11816/c
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Matches
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SEQ ID NO 11816
LENGTH: 7561
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11816, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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ORGANISM: Human
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nilarity 55.3%;
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Pred. No. 0.25;
0; Mismatches 5
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Pred. No. 0.14;
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US-09-949-016-13895
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Patent No. 5856454
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SOFTWARE: PRETSEQ FOR WINDOWS Version 4.0
SEQ ID NO 11895
LENGTH: 7562
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Best Local Similarity
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                    COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
PILING DATE: 09-SEP-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                         ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GONZALEZ, Frank J.

APPLICANT: FERNANDEZ-SALGUERO, Pedro
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
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Pred. No. 0.25;
0; Mismatches
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:

NAME: Smith, Timothy L.

REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 15280-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                 ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FERNANDEZ-SALGUERO, Pedro
TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN
TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                               APPLICATION NUMBER: US/08/991,942 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                 CLASSIFICATION:
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Steuart Street Tower, One Market Plaza
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Pred. No. 1.8;
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2394

TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 4447 base pairs

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US-09-949-016-11745
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, NAME/KEY: misc feature
; LOCATION: 1.4447
; OTHER INFORMATION: /product= "Pig DPD"
US-08-991-942-3
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Best Local Similarity
Matches 68; Conserv
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

FULB REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14
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Best Local Similarity
Matches 82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 207012
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                           2712
                                                                                                                                  2652 ACCCCCTTCCCCCCGCGGGAAGAACAGGAGCTAGGTAGGCCCTGGGTTTGGGGCCCTA
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nilarity 53.1%;
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88..3162
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                                                                                                                                                                                                         Score 32; DB 4; Length 36180; Pred. No. 5.5; 0; Mismatches 60; Indels
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Search completed: September Job time: 87.4384 secs 1, 2005, 07:07:09

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Result
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Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 s
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AY095345
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                        AX163782 Sequence
L22979 Rat insulin
BC078889 Rattus no
AY095345 Papio anu
AX409747 Sequence
M74867 Human insul
G19994 sWSS752 Eri
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X67493 M.musculus
AL607124 Mouse DNA
BC013345 Mus muscu
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AX401392 Sequence
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AX827271 Sequence
AY434089 Homo
AC091524 Homo
                  M59316 Human insul
                                                                                                                                                                                Description
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C 45	C 44	43	C 42	c 41	C 40	c 39	c 38	37	w	c 35	C 34	33	c 32	c 31	30	29		c 27			C 24	23	N	c 21	c 20
36.6	36.6	36.8	36.8	σ	37.8	37.8	37.8	40.2	40.2	40.2	40.4	44.4	47.4	47.4	52	54.4	55.2	55.2	55.2	55.2	55.2	60.8	62.2	62.2	62.2
11.4	11.4	11.5 3	11.5 3	11.5 3	11.8	11.8	11.8	5	12.5	12.5	12.6	13.8	14.8 2	14.8	16.2	16.9	17.2	17.2	17.2	17.2	17.2		19.4 2	19.4 1	19.4 1
1678	1678	349442	348997	348525	7061	7061	7061	133525	13322	8409	415	1480	231241	2717	539	895	13011	13011	13011	194	194	448	200935	189932	41539
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AK054581	AX713325	BX640447	BX640427	BX640428	AX348680	AX345899	AX251887	AL713999	AY316591	HSU47654	HSPYKINPR	RATIGFBP1	AC097039	RATPKRL1	G67173	HUMIGFBPB1	RNLPKG	AX827302	E14395	AR175909	A57715	G67139	AC148834	AC146117	AC146152
AK054581 Homo sapi	AX713325 Sequence	BX640447 Bordetell	BX640427 Bordetell	BX640428 Bordetell		AX345899 Sequence	AX251887 Sequence	AL713999 Human DNA	AY316591 Homo sapi	U47654 Homo sapien	Z18922 H.sapiens D	M89791 Rattus norv	AC097039 Rattus no	M17088 Rat pyruvat	G67173 IGFBP1 5'A	M23592 Human insul	X05684 Rat L-PK ge	AX827302 Sequence	E14395 gDNA encodi	AR175909 Sequence	A57715 Sequence 1	G67139 IGFBP1 X1.1	AC148834 Pan trogl	AC146117 Pan trogl	AC146152 Pan trogl

ALIGNMENTS

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REFERENCE
AUTHORS
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RATILGFZ
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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Best Local Similarity
Matches 218; Conserv
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Unterman,T.G., Lacson,R.G., McGary,E., Whalen,C.
Biochem. Biophys. Res. Commun. (1991) In press
Original source text: Rattus norvegicus (strain smale adult liver DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin-like growth factor.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Rattus norvegicus insulin-like
M84484
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Mammalia; Eutheria;
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CCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGG
                                           CTGACAATCATTAACCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAG 212
                                                                                                    TGTGCGGAGCTCACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC
                                                                                                                       TGCGCCCATGTCACAAGCAAAACCAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC 152
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="genomic_DNA"
/mol_type="genomic_DNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
/iex="male"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                    /tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                            66.8%;
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Rodentia;
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Pred. No. 4.6e-53;
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                                                                                            Bryant, N., Black, D., Blankenbudy, K., Bryth, P., Center, R., Carderon, R., Center, K., Cavasos, I., Ceasar, H., Center, R., Chen, Z., Chu, J., Charderon, J., Charderon, P., Chen, Z., Chu, J., Charderon, C., Cockeell, R., Cox, C., Coyle, M., Crea, A., D'Souza, L., Davila, M.L., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K., Deval, A., L., Davis, C., Despor, R., Duran, R., Durbin, K., Daval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Hernandez, J., Gunarathe, P., Halland, W., Handl, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, N., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Jackson, A., Jackson, A., Jackson, A., Jackson, L., Jacob, L., Jang, H., Johnson, B., Johnson, D., Jackson, A., Jackson, A., Jackson, A., Jackson, A., Lovas, J., Liu, J., Loulseged, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Loulseged, H., Lovado, R., Martinez, B., Malloy, K., Mangum, A., Maheshwari, M., Mahindarthe, M., Mahindar, R., Martinez, B., Malloy, K., Mangum, A., Mannes, S., Munidasa, M., Norris, S., Naceleneh, D., Okwoonu, G., Olarnpunssegoon, A., Pal, S., Parks, K., Pasternak, S., Pall, H., Martin, R., Railly, B., Reilly, M., Ren, Y., Reeves, K., Regter, M., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reeves, K., Regter, M., Richards, S., Shen, H., Shetty, J., Sheartes, W., Scherer, S., Soretle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Sisson, L., Wonzis, S., Wanders, M., Sochere, S., Scherer, S., Steon, J., Valas, R., Vera, J., Valas, R., Vera, J., Valas, R., Walzer, M., Jang, J., Zhou, X., Tepos, Z., Usani, K., Mang, J., Zhou, J., Zhou, X., Tepos, S., Matsen, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny, D. Marie., Metzker, M. Lee., Allen, C., Allen, H., Alsbrooks, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC136382.1 GI:2
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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itus norvegicus clone CH230-97018,
, 63 unordered pieces.
36382
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  Genome Sequencing Consortium
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3, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benahmed, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baylor Plaza, Houston, TX 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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(see http://www.lsgsc.bcm.ttc.edu/docs/Genbank draft data.h

NOTE: This is a 'working draft' sequence. It currently

consists of 63 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; version 0.990329
Consensus quality: 135613 bases at least Q40
Consensus quality: 140849 bases at least Q30
Consensus quality: 145680 bases at least Q20
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Center clone name: CH230-97018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Mohn, K.L., Waddle, J.R. and Taub, R.
Comparison of mouse and human IGFE
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Mus musculus
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Lee, J., Greenbaum, L., Haber, B.A., Nagle, D., Lee, V., Miles, V.,
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/mol types "genomic DNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="WW2.1"
/cell_type="fibroblast"
/cell_type="fibroblast"
/cone_ilb="genomic, lambd
/dev_stage="embryo"
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/product="insulin-like growth factor
/protein id="CAA47832.1"
/db_xref="GI:52700"
/db_xref="GOA:P47876"
/db_xref="UniProt/Swiss-Prot:P47876"
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                                                                                                                                                                                                                                                                            AL Submitted (11-ARR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk On Apr 12, 2002 this sequence version replaced gi:19847866. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG.
Mus musculus
Mus musculus
                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
AL607124
                                                                                                                                                                                                                                                                 database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oliver, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL607124.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCTGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGACAATCATTAACCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submission
/organism="Mus musculus'
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MPEFLTVVSWPFLILLSFQIGVAAGAPQPWHCAPCTAERLGLCPPVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGASLPEPAAPATSTLFSSQHE"
                                                                                                           Location/Qualifiers
                                                                                  .192843
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Pred. No. 2.1e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192843 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp DNA linear ROD 11-APR-2002
RP23-20C9 on chromosome 11, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
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BC013345
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                                                                                                                                                                                                                                                                                                                                                                                                     RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Wadan, A., Kodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                            Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC013345 1569 bp mRNA linear ROD Mus musculus insulin-like growth factor binding protein (cDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                       Contact: MGC help desk
                                                                                                                                                                                   Gene Collection (MGC), Canc
Institute, 31 Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                             NIH-MGC Project URL: http://mgc
                                                                                                                                                                                                                                                                                        Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences
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/clone_lib="RPCI-23"
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                                                                                                                                                                                   Cancer Genomics Office, National rive, Room 11A03, Bethesda, MD 20
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Pred. No. 2.
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1, mRNA
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Best Local S
Matches 103
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                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                              20
Li,Y., Klimanis,D. and Hallenbeck,J.M.
Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                                                                                                                                       Spermophilus tridecemlineatus protein 1 (IGFBP1) mRNA, comp. AY560836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 1B Row: 1 Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.systemsbiology.org
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Anup Madan, Jessica Fahey, Amy Sanchez and Michelle Whiting
                                                                                                                                 Spermophilus tridecemlineatus (thirteen-lined ground squirrel) Spermophilus tridecemlineatus
                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                        AY560836.1 GI:45505308
                                                                                                                                                                                                                                                              AY560836
                                                                           Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                         CACACGGCCATCTGCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTG
                                                                                                                                                                                                                                                                                                                                                    CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tränalation="MPEFLTVVSWPFLIILLSFQIGVAAGAPQPWHCAPCTAERLGLCP
PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQCLSCRALPGEBRPLHALTRG
OGACVPEPAAPATSTLSSGQHEEAKAAVVSADELSESEBTMTEEQLLDSFHLMAPSRED
OPILMNAISTYSSMMAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVHN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="insulin-like growth factor binding /protein_id="AAH13345.1" /db xref="GI:15426483" /db xref="GI:15426483"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="LocusID:16006"
/db_xref="MGI:96436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Igfbp1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="MGC:14075 IMAGE:4161889"
/tissue_type="Liver, normal. 5 m/
/clone_Tib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 98.2; DB 10; Pred. No. 2.7e-18;
                                                                                                                                                                                                                                     1507 bp mRNA linear leatus insulin-like growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                            complete
                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Sciuridae; Sciurinae;
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AX401932
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Local Similarity
                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                     1500 bp
Sequence 1608 from Patent WO0210453
AX401932
                                                                                                                                Gene
                                                                                                                                                      Patent:
                                                                                                                                                                                            Elashoff, M.R.
                                                                                                                                                                                                                  Mendrick, D.,
                                                                                                                                                                                                                                                                                                                                                                                     AX401932.1 GI:21338112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-FEB-2004) StrokeBranch, NINDS/NIH, Bethesda, MD 20892, USA
                                                                                                                                                                        Molecular toxicology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                            Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGCCCATGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GCCACTGCCAGCTGCCCAGAGAGCATTGACCACCTGTCC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCACACGCCATCTGCCCAGAGAGCTGTGACCACCACTTC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCACCCAGCAAGCATCGTGCACTGCCCACGGCGACTCAGAATTGGACACCTATCAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATGGCCAGCCAGCATGGTCCACTGCCCGGCCGAGACACAAACCCCAGCGAGCATTGAACA
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                                                                                                                           Logic,
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                                                                                                                                             WO 0210453-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MPEVPAAGLWPFILLLAVQVSTVASSTQPWHCAPCSAEKLALCP 
PVPSSCPELSRPAGCGCCPMCALPLOAACGVATARYARGLSCRALPGEPRPLHALTRG 
QGACVPEPATPTASGLSSIEKEEAKASMVPBRVPPESAEMTEEQLLESFHLMASSSED 
QPILWWAISTYKSMRAREWADIKKWKQPCRRELYKVLERLAKAQQKAGESIYKFYLPW 
CNKNGFYHSKQCETSLDGEAELCWCVYPWSGRRIPGSLEIRGDPNCHQYFNVQN"
                                                                                 Location/Qualifiers
/note="EMBL/GenBank Accession No. NM_013144"
                   organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="insulin-like
/protein_id="AAS67029.1
/db_xref="GI:45505309"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Spermophilus/mol_type="mRNA"
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                                                                                                                                Inc.
                                                                                                                                                                                                             Porter, M.W., Johnson, K.R.,
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                                                                                                                              (US)
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Pred. No. 1.3e-12;
0; Mismatches 58;
                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                               Castle, A.L.
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Best Local S
Matches 77
                                                              JOURNAL
MEDLINE
PUBMED
                                                                                                                 AUTHORS
TITLE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: F. HOFFN
                                                                                                                                                                                            M58634.1 GI:204732
IGF binding protein-1.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                                                      Mohn, K.L., Melby, A.E., Tewari, D.S., Laz, T.M. and Taub, R
The gene encoding rat insulinlike growth factor-binding
is rapidly and highly induced in regenerating liver
mol. Cell. Biol. 11 (3), 1393-1401 (1991)
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                15
Rat IGF binding protein-1
M58634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX827271 1500 bp
Sequence 5 from Patent EP1344834.
AX827271 GI:39837360
                                                Original
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
                                                                                                                                                        Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ess,F., Suter-Dick,L. and Wolf,D. thods for the toxicity prediction tent: EP 1344834-A 5 17-SEP-2003; HOFMANN-LA ROCHE AG (CH)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                   source text: Rat, cDNA to
1. .1500
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                   Location/Qualifiers
                         .1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.8%;
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98.7%;
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Rodentia;
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Pred. No. 8.9e-12;
0; Mismatches 1;
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Pred. No. 8.9e-12;
D; Mismatches 1
                                                                                                                                                                                                                                                            1500 bp mRNA
1 (rIGFBP-1) mRNA,
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Sciurognathi; Muridae;
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; Murinae;
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AX163782
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AX163782
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                                                                                                                     Similarity
                                                                                                                                                                                                                                                                   Method of identifying toxic agents ungene expression in liver Patent: WO 0138579-A 46 31-MAY-2001; Curagen Corporation (US)
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                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC 298
                           CACTICCGCTACTAGCTA 316
                                                          CACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
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                                                                                                                     Conservative
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46 from Patent WO0138579.
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235. .975
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PVPASCPEISRPAGCGCCTCALPLCAACGVATARCACACLSCRALDSFERFLHALTRG
QGACVLEPAAPATSSLSGSQHEEAKAAVASSDELASSPEMTEEQLLDSFEHVAAPSFED
QDILWMAISTYSSWRAAEITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
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                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                          /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="IGF binding protein-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="IGF binding
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/db_xref="GI:204733"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="regenerating liver"
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160._.978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Fisher"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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98.7%;
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Rodentia;
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Pred. No. 8.9e-12;
0; Mismatches 1
                                                                                                                    Score 76.4; DB 6;
Pred. No. 9.5e-12;
D; Mismatches 1;
                                                                                                                                                                                                                                                                                                              agents using nsaid-induced differential
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RESULT 11 RATIGFBA

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Best Local Similarity
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239 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dideoxy sequencing and structural analysis of growth factor binding protein-1 gene Biochim. Biophys. Acta 1218 (1), 95-98 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
Rattus norvegicus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On NOV 30, 1995 this sequence version replaced gi:385167 Original source text: Rattus norvegicus (strain Sprague-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA.
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PVPASCPEISRPÄGCGCCPTCALPLGAACGVATÄACAQGLSCRALPGEPRPLHALTRG
QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
                                                                                                                                                                                               3003. .4089
/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                           CNKNGFYHSKQCETSLDGEAGLCWCVYPWSGKKIPGSLETRGDPNCHQYFNVQN"
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/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                              1850. .2034
/gene="IGFBP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MPEFLTVVSWPFLILLSFQVRVVAGAPQPWHCAPCTAERLELCP/
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                                                                                                                                                                                number=
                                                                                                                                                                                                                                                gene="IGFBP-1"
                                                                                                                                                                                                                                                                              number-2
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                                                                                                                                                                                                                                                                                                                                                                                             gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="liver"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Rattus norvegicus"
/mol_type="genomic DNA"
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98.7%;
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                                                Score 76.4; DB 10;
Pred. No. 9.5e-12;
0; Mismatches 1;
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Milahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.M., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 114 Row: e Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6981079.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Director MGC Project.

Direct Submission

Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) National Cancer Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodrique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus insulin-like growth factor binding protein 1, mRNA (cDNA clone MGC:93595 IMAGE:7129185), complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/organism="Rattus norvegicus"
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RESULT 13
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TITLE
JOURNAL
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Best Local Similarity
Matches 66; Conserv
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gene
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1 (basses to 3886)

Kim,J.J., Taylor,H.S., Akbas,G.E., Foucher,I., Trembieau,A., Kim,J.J., Taylor,H.S., Akbas,G.E., Foucher,I., Trembieau,A., Kim,J.J., Taylor,B.A.T. and Unterman,T.G. Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                   Direct Submission
Submitted (11-APR-2002) Department of Obstetrics and Gynecology,
Submitted (11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papio anubis (olive baboon)
Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY095345

Papio anubis insulin-like growth factor binding protein-1 (IGFBP-1)
                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 3886)
Kim, J.J., Jaffe, R.C. and Fazleabas, A.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY095345.1 GI:20853764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATCTA 67
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/protein_id="AAH78889.1"
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/db_xref="RATMAP:44422"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="LocusID:25685"
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/db_xref="RGD:2872"
142...960
                               /organism="Papio anubis"
/mol_type="genomic DNA"
/db_xref="taxon:9555"
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MGC:93595 IMAGE:7129185"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Igfbp1"
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       .>3886
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Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 2394 from Patent WO0229103
AX409747
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                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                 ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC------
                                                      CACTTC 304
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insulin-like growth factor binding protein.
Homo sapiens (human)
Homo sapiens
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Human insulin-like growth factor binding protein (hIGFBP1) gene,
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36.6	36.6	36.6	36.6	36.6	36.6	36.6	36.8	36.8	36.8	38.8	47.2	59	60.8	60.8	61.6	61.8	62.8	64.4	65.4	67.4
11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.5	11.5	11.5	12.1	14.7	18.4	18.9	18.9	19.2	19.3	19.6	20.1	20.4	21.0
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BX360059	CN402794	CD635412	CD635411	CN402792	CN402791	CN402790	AL208895	CV014020	BF829782	BU684425	AZ840793	AA060360	CR595377	CR621807	AW916227	BB604790	AA105355	CK473709	CK472246	AA674302
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ALIGNMENTS

RESULT 1 BF236974 LOCUS ACCESSION VERSION ORIGIN FEATURES COMMENT REFERENCE SOURCE ORGANISM KEYWORDS DEFINITION TITLE AUTHORS JOURNAL source Email: cgapbs-r@mail.nih.gov
Tlssue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9443 row: j column: 02
High quality sequence stop: 581.
Location/Qualifiers Unpublished (1999) Contact: Robert Strausberg, Ph.D. mRNA sequence. BF236974 National Institutes of Health, Mammalian Gene Collection (MGC) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1013) Mus musculus BF236974 1013 bp mRNA linear EST 14-NOV-2000 602026605F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4161889 5', NIH-MGC http://mgc.nci.nih.gov/. Mus musculus (house mouse) BF236974.1 GI:11150891 /db_xref="taxon:10090"
/clone="IMAGE:4161889"
/lab_host="PH108 (T1 phage-resistant)"
/clone_lib="NCI CGAP_Li9"
/clone_lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SpORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP_Library." organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" . .1013 Length 1013; be Mue .

Result No.

Score

Length DB

BF236974

BF236974 602026605 Description

AI790802 AI528304 AI196154 AI785039 CO573026

AI529939 CA478518

AI785818 AI196314 AI530146 AI098594 AI530313

BY783538 BY783538 BY794229 BY794229 BY771317 BY771317 AI785818 ui78h05.y AI196314 ui71a07.y AI530146 ui89160.y AI098594 ue31e07.y AI098594 ue31e07.y AI530313 ui97160.y AI529939 ui87c0.y CCA478518 AGENCOURT AI790802 uk28b10.y AI1528304 ui69508.y AI196154 ui69508.y

CV127049 CO560662 CO575629 CV117001

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CV117001 AGENCOURT
CV117001 AGENCOURT

BB660958 CD561711 AI892189

BB660958 BB660958 CD561711 B0435D02-

S Query Match
Best Local Similarity
Matches 103; Conserv 206 TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTG 265 Conservative 30.6%; Score 98.2; DB 2; Pred. No. 2.6e-17; 0; Mismatches 8; 8 0 Gaps

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RESULT 2
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
Tel: 81-45-503-9222
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BY783538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY783538
BY783538 RIKEN full-length enriched, 17.5 days embryo
Mus musculus cDNA clone L930176D05 5', mRNA sequence.
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TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                 ATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                                       ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
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                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                        tissue_type="whole body"
/dev_stage="17.5 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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92.9%;
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                                                                                                                                                               0,
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1 (carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sigahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hiirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Kavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Pavan, W., Okazaki, Y., Wells, C., Hume, D.A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6R) 173-1789 (2003)
                                                                                                                                                                                                             92;
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The Institute of Physical and Chemical Research (RIKEN)
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TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                                   TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                           ATGGTCCACTGCCCGCCGAGACACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                                                                       ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/strain="C57BL/6J"
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92.9%;
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Rodentia;
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Pred. No. 2.1e-14;
D; Mismatches 7
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d, 17.5 days embryo whole body
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RESULT 5
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Best Local Similarity
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                                                                                                                                                                                                                   62
                                          AI785818 401 bp mRNA linear EST 02. ui78h05.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for
                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikwa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Favan, W., Aldinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayushizaki, Y. Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6B), 1273-1289 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
insulin-like
AI785818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web
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354 bp mRNA linear EST 23-MAR-2
BY771317 RIKEN full-length enriched, 17.5 days embryo whole body
mus_musculus cDNA clone L930052G15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (house mouse)
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                                                                                                                                                                                                                   TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                                                                                                                                                                                                                                                                                             ATGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTC
                                                                                                                                                                                                                                                                                                                                                          ATGGTCCACTGCCCGCCGAGACACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                                                                                                                                                                                                                         TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 354)
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone ____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="L930052G15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
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                      growth
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                                                                                                                                                                                                                                                                                                                                                                                                                                27.4%;
92.9%;
                      factor binding (MOUSE);, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                         0,
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Pred. No. 2.1e-14;
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DEFINITION

mRNA for insulin-like

growth factor binding

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RESULT 6
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LOCUS
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                                                                                                                                                                                                                                                  279 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
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                                                                                                                                                                                                                                                                                           1
                                                                                                                                                                                                                                                                                                                                                                                                     91;
ARI196314 ARO DE MRNA linear EST 14-OCT-19 ui71a07.y1 Sugano mouse liver mlia Mus musculus CDNA clone IMAGE:1887828 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rax: 311 %00 2020
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other ESTs: ui78h05.xl
Contact: Marra M/WashU-NCI Mouse EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Pitter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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EST.
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Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llnl.gov)
MGI:972893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St.
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                                                                                                                                                                                                                                                                                                                               TGGTCCACTGCCCGGCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCT
                                                                                                                                                                                                   GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3'primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the CDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA
strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                            27.0%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86.8; DB 1
Pred. No. 4.2e-14
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                                                      EST 14-OCT-1998
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RESULT 7
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                                                                                    DEFINITION
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AI530146
706 bp mRNA linear EST 18-MAR-19 u189f09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            91;
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1 (bases 1 to 480)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
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Contact: Marra M/Mouse EST Project
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AI196314.1 GI:3748920
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/note="Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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AI530146
AI530146.1
             AI098594 765 bp mRNA linear kST 20-
ue31e07.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
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Email: mouseesfewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL; contact the
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1 (bases 1 to 706)
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/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACCTGTGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
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constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
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sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/clone="IMAGE:1889609"
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/strain="C57BL"
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Pred. No. 4.7e-14;
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                A1530313
785 bp mRNA linear EST 18-MAR-1999 u191f01.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889785 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
sequence
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//note="Organ: liver; Vector: pMELBS-FL3; Site 1: DraIII
/(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMELBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
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constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/clone="IMAGE:1481988"
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92.9%;
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Pred. No. 4.8e-14;
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RESULT 10
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A1529939
799 bp mRNA linear EST 18-MAR-1: ul97c09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889392 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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The WashU-NCI Mouse EST Project 1999
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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//note="Organ: liver; Vector: pME185.FL3; Site 1: DraIII
(CACCMTGTG); Site 2: DraIII (CACCMTGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185.FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG), XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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| lab_host="DH10B"
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strain="C57BL"
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92.9%;
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Pred. No. 4.8e-14;
); Mismatches 7
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RESULT 11
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                   AGENCOURT 10789306 NIH_MGC_152 Mus musculus cDNA clone IMAGE:6766752 5', mRNA sequence. CA478518 CA478518.1 GI:24936188
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The WashU-NCI Mouse EST Project 1999
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Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                            CA478518
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 799)
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//Clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pwEl8S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pwEl8S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/clone="IMAGE:1889392"
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/lab_host="DH10B"
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/strain="C57BL"
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|mol type="mswa"
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92.9%;
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Pred. No. 4.8e-14;
0; Mismatches 7;
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                          Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y. Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Sch Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCa Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Al790802 848 bp mRNA linear EST 02-0 uk28b10.71 Sugano mouse kidney mkia Mus musculus CDNA clore IMAGE:1970299 5' similar to gb:x881579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
Unpublished (1999)
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 848)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri 1 (Dases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 136
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/db xref="caxon:10090"
/clone="IMAGE:6766752"
/clone="IMAGE:6766752"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 152"
/clone lib="NIH MGC 152"
/note="Organ: Liver; Vector: pDONR201; Site_1: attP2;
/clone lib="NIH MGC 152"
/note="Torgan: Liver; Vector: pDONR201; Site_1: attP2;
/clone lib="NIH MGC 152"
/clone lib="NIH
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92.9%;
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Pred. No. 4.9e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
                                                                                                              Cardenas, M., McCann, R.,
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Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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A1528304

B52 bp mRNA linear EST 18-MAR-19 ui95g10.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890210 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH PACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1. (bases 1 to 852)
                                                                                                                                                                                                                                                                                                  sequence.
AI528304
AI528304.1 GI:4442439
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                       Mus musculus
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//clone lib="Sugano lib sugano constitute of praili adaptor [Garcargargaranded cona de distinct Draili sites of the pME188-FL3
//cloned into distinct Draili sites of the pME188-FL3
//cloned into distinct Draili sites of the pME188-FL3
//cloned into distinct Draili sites election was
performed to exclude fragments <1.5kb. Library
//constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5, end primer CTTCTGCTCTAAAAGCTGCG and 3, end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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Pred. No. 4.9e-14;
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AI196154

JAMUS MUS MUSCULINE CDNA CLONE

IMAGE: 1887663 5' similar to gb: M59316 rnal INSULIN-LIKE GROWTH

FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb: X81579 M. musculus
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                    1 (bases 1 to 605)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                     Mus musculus (house mouse)
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                               AI196154.1
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: custom primer used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII (CACCATGTGTG); Site_2: DraIII (CACCATGTGTG); 1st Strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG] digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library conserructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev_stage="adult"
| lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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92.9%;
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Pred. No. 4.9e-14;
); Mismatches
                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                      Dietrich, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Site_1: DraIII
1st strand cDNA
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REFERENCE
AUTHORS
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VERSION
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AI785039
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Best Local S
Matches 90
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JOURNAL
                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 380)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Materston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                         Al785039 ARNA linear EST 02-
ui73a06.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888018 5' similar to gb.X81579 M. musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                  Mus musculus
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                             AI785039.1 GI:5332755
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Location/Qualifiers
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Seq primer: custom primer used
                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTCCACTGCCCGCGAGACACACACCCAGCGAGCATTGAACACTGCACACGGTCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Sugano mouse liver mlia"
//note="Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII
/(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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Pred. No. 1.3e-13;
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les 87; Conserv
                                                                                                                               282 CAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 316
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Fax: 314 286 1810
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                                                                                                                                                                                                                             TCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCC
                                                                                                                                                                                 TCCACTGCCCGCGGAGACACACCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Sugano mouse liver mlia"
//clone lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pMB18S-FL3; Site 1: DraIII
/(CACCHTGTG); Site 2: DraIII (CACCHTGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
September
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/db_xref="taxon:10090"
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lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE:1888018"
|sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                    25.6%;
  2005, 06:56:49
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                            Score 82.2; DB 1;
Pred. No. 8.8e-13;
0; Mismatches 8;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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2
                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                       321
321
219.4
219.4
219.4
                                                                                                                                                Score
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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length: 2000000000
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Match
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/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

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e 844,	equence 492, A	equence 150407	equence 150407,	e 25564,	e 25563	e 25562,	equence 25564,	25563,	25562,	1, Ap	e 79185	e 79162,	e 7, App	6, Appl	e 17905,	equence 5746	e 76, App	equence	e 164336	equence 5461, A	e 22	82	equence 9,	148,	970	□	ω	ب	o N	Sequence 36, Appl	_	_	e L	2	e _	equence 73, App	Sequence 5, Appli

ALIGNMENTS

RESULT 1 US-09-972-916A-4

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SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
                                                                                                                         Query Match 100.0%; Score 321; DB 9; Best Local Similarity 100.0%; Pred. No. 9.2e-100; Matches 321; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                     FEATURE:
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                                                                     TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCCGTGCGCCCCATGTACACTGGG
TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG 60
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Sequence 5, Application US/09972916A

Patent No. US20020107198A1

GENERAL INFORMATION:
APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 5
LENGTH: 372
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local
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                                                                                                CTTCCGCTACTAGCTAGCCGC 321
                                                                                                                                                     TACACTGGGGGCCAGAGTCCAGGAAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG
                                                                               CTTCCGCTACTAGCTAGCCGC 372
                                                                                                                                 CAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCACCA
                                                                                                                                                                                      CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
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APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
PILE REFERENCE: US 129/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 6

LENGTH: 423
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GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 270
TYPE-CANATA
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Best Local Similarity 99.5%;
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                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                       Local Similarity
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                                 263
                                                                                                                       101 TGTCACAAGCAAAACCAAACTTATTTTGAACACGGGGATCCTAGCACGCCTGCCCTGACAAT 160
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221 GTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGC 280
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Pred. No. 7.5
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Pred. No. 6.7e-65;
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RESULT 6
US-09-972-916A-6/c
US-09-972-916A-6/c

Sequence 6, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
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                                                                    ; OTHER INFORMATION: Synthesized US-09-972-916A-6
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US-09-972-916A-2
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TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR PILE REFERENCE: US 1292/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
LENGTH: 219
TYPE: DNA
ORGANISM: Rattus norvegicus
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Query Match 32.1%; Score 103; DB 9; I Best Local Similarity 100.0%; Pred. No. 6.9e-25; Matches 103; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REPERENCE: US 192/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR PILLNG DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                                                                                  LENGTH: 423
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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100.0%; Pred. No. 8.7e-65;
tive 0; Mismatches 0;
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                               Length 423;
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US-10-388-934-5

Sequence 5, Application US/10388934
Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura

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US-09-917-800A-1608
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PRIOR FILLING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILLING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILLING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/292,457
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILLING DATE: 2001-06-19
PRIOR FILLING DATE: 2001-07-09
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Best Local
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SEQ ID NO 1608
LENGTH: 1500
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5018-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mendrick, APPLICANT: Porter, N
                                                                                                                                                                                                                                                                                                                               ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013144
                                     299 CACTTCCGCTACTAGCTA 316
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                                                                                                                                          239 CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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CACTTCCGCTACTATCTA 85
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Castle, Arthur
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                                                                                              CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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98.7%;
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                                                                                                                                                                                    Score 76.4; DB 9;
Pred. No. 1.3e-15;
0; Mismatches 1;
                                                                                                                                                                                                                                 Length 1500;
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                                                                                                                                                                                               US-10-191-803-73
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                                                                                                                                                                                                                                                                                  SEQ ID NO 73
LENGTH: 1500
                                                                                                                            Matches
                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
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CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR PILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/303,819 PRIOR FILING DATE: 2001-07-10
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CURRENT FILING DATE: 2002-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                 ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                     TYPE: DNA
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les 77; Conserv
                     299
                                                                         299 CACTTCCGCTACTAGCTA 316
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                                                                                                                                            Similarity
CACTTCCGCTACTAGCTA 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASTLE, Arthur
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98.7%;
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                                                                                                                        Score 76.4; DB 17;
Pred. No. 1.3e-15;
0; Mismatches 1;
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Pred. No. 1.
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US-09-880-107-2393
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US-10-152-319A-1613
                                                      Sequence 2393, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                  APPLICANT: Gene Logic, Inc. TITLE OF INVENTION: Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
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PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/152,319A CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Elashoff, Michael TITLE OF INVENTION: Molecular Toxicology Modeling FILE REFERENCE: 44921-5089-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mendrick, Donna APPLICANT: Porter, Mark
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2221
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PRIOR APPLICATION NUMBER: US 60/303,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-10-22
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                                                                                                                                                                                                                                                                                       CACTTCCGCTACTATCTA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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98.7%;
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Pred. No. 1.3e-15;
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                    Profiles
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FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1484
LENGTH: 6128
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-756-149-1484
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CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2393
LENGTH: 6128
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US-10-756-149-1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 156
                                                                                                                                                                                                                                                Matches 156;
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Genbank Accession No. US20020142981A1 M74587-09-880-107-2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Alb
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                                                                                                                                                                                                                                                                            Local Similarity
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                            ACACTCAGCTCCTAGCGTGCGGCGCTGCCAATCATTAACCTCCTGGTGCAAGTGGCGCGG
                                                                                                                                  CCGCTCC
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Pred. No. 3.8e
0; Mismatches
                                                                                                                                                                                                                                          Score 63.8; DB 22;
Pred. No. 3.8e-11;
0; Mismatches 72;
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                ; Sequence 160, Application US/10893315
; Publication No. US20050147987A1
; GRNERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN (
TITLE OF INVENTION: WITH TYPE II DIABETES ;
TITLE OF INVENTION: USES THEREOF
; TITLE OF INVENTION: USES THEREOF
; TITLE OF INVENTION: USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT APPLICATION UNMBER: US/10/893,315
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PRIOR APPLICATION NUMBER: 60/231,397
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WESULT 13
US-10-893-315-126
US-10-893-315-126
Sequence 126, Application US/10893315
Publication No. US20050147987A1

Publication No. US20050147987A1

GENERAL INFORMATION:
FORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILLE REFERENCE: CL000786
CCURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR APPLICATION SEQ ID NOS: 2172
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 126
LENGTH: 9173
TYPE: DNA
CREAMING. USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.9%; Best Local Similarity 63.2%; Matches 156; Conservative
CCGCTCC 2080
                                                 CCACTTC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----CATCCAGCGAGCATCTGCCGCCGCGCGCCGCCACCCTCCCAGAGAGCACTGGCCA
                                                                                                                                                                                                          CCTGTGCCCTTTATAAGGTGCGCGCTGTGTCCAGCGAGCATCGGCCACCGCCATCC----
                                                                                                                                                                                                                                                            AGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGA
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Pred. No. 4.3e-11;
0; Mismatches 72;
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IN KNOWN GENES ASSOCIATED DIABETES AND OBESITY, METHODS OF DETECTION AND

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CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: Patentin version 3.1
SEQ ID NO 36
LENGTH: 13011
TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-36
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US-10-388-934-36/c
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Publication No. US20040005547A1
GENERAL INFORMATION:
APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
                                                                                                                                                         Query Match
Best Local Similarity
Matches 60; Conserv
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3028 CGCCCATG 3021
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Search completed: September Job time: 944.893 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Listing first 45 summaries
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US-08-945-140-1
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 30, Appl
1, Appl
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1138, App
138, App
138, Ap
2153, Ap
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13895, A
29006, A
13895, A
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1363, Appl
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US-09-949-001-36
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	15398, /	11765, 4	11859, 1	16640, A	173899,	2808, Ap	, Appli	12, Appl	30284, A	805, App	17016, A	1241, Ap	4899, Ap	13083, 7	1341, Ap	169693,	169692,	TOSTO, W

ALIGNMENTS

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; TYPE: DNA
; ORGANISM: Human
US-09-949-001-30
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Patent NO. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH. 0173
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Best Local Similarity
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CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
RUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 9174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08945140 Patent No. 6309878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
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Best Local Similarity
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHEN, Ruibuan
APPLICANT: DOIRON, Bruno
APPLICANT: KAHN, Axel
TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 10
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,140
                                   FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/04558
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 19426
                                                                                                                                                                                                                                                                                              STREET: 500 Arcola CITY: Collegeville
                     FILING DATE:
                                                                                                                                                                                                                                                                                    STATE:
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APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                     500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                       Rhone-Poulenc Rorer Inc.
                     14-APR-1995
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RESULT 4
US-08-791-849A-14/c
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                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Makoto
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791
FILING DATE: January 30, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (610) 454-3808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                          REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44
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LENGTH: 194 base pairs
TYPE: nucleic acid
                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Makoto MURASE et al.
TITLE OF INVENTION: Method for Increasing Storage
TITLE OF INVENTION: Lipid Content in Plant Seed
NUMBER OF SEQUENCES: 15
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NAME: Savitzky Esq., Martin F. REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: EX950
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 20005
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Local Similarity 88.2%;
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                                    nucleic acid
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                                                    13011 base pairs
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805 Fifteenth Street, N.W., #700
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Pred. No. 1.6e-08;
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RESULT 6
US-09-949-016-17205/c
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; SOFTWARE: FRETSEQ for Windows Version 4.0
; SEQ ID NO 11786
; LENGTH: 15108
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
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US-09-949-016-11786/c
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US-08-791-849A-14
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 60
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Best Local Similarity
Matches 48; Conserv
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11786, Application US/09949016 Patent No. 6812339
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NAME/KEY:
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NAME/KEY:
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Local Similarity 88.2%;
les 60; Conservative
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                                                                                                                                                                                                                 Conservative
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join(3194..3218, 3766..3948, 5917..6008,
6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(3212..3218, 3766..3948, 5917..6008,
6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..8077
9298..9479, 10163..10269)
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78.7%;
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                                                                                                                                                                                                             Score 40.2; DB 4; Length 15108; Pred. No. 0.011; o; Mismatches 13; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR RILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 17205
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APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ. ID NOS: 172
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US-09-949-016-17205
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; SEQ ID NO 138
; LENGTH: 3054
; TYPE: DNA
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 138, Application US/09484970B Patent No. 6426186 GENERAL INFORMATION:
                                                                                                                                                       Matches
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TITLE OF INVENTION: BOTHMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 336987.1CB1
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2417
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                                    62 GCCAGAGTCCAGGAACCACGGGAGTGCCCCG 92
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                                                                        ACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGG
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                                                                                                                                                     Conservative
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                                                                                                                                                                     11.4%;
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78.7%;
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                                                                                                                                                                     Score 36.6; DB 3; Pred. No. 0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40.2; DB 4; Pred. No. 0.011;
                                                                                                                                                       Mismatches
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                                                                                                                                                                                       Length 3054;
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RESULT 8

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US-09-949-016-19194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 73784, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                            SEQ ID NO 73784
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19194
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                                                                                         Matches
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                        ENGTH: 601
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                                                                                       Local Similarity 55.3
les 68; Conservative
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                             181 CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA 240
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    CCAGGCCTTCCTGGGGGCGCTGTTCCTCCATCCAGCTTAGCCACCTGCCAGGTTAGGCC
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                                                                                                         10.9%;
                                                                                  Score 35; DB 4; Pred. No. 0.14; 0; Mismatches
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Pred. No. 0.14;
0; Mismatches
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                                                                                                                               Length 601;
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RESULT 11
US-09-949-016-74/c
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US-09-949-016-2153/c
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           APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING LATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2153
LENGTH: 2393
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                        Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 74, Application US/09949016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CRICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL001307
LENGTH: 2408
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GENERAL INFORMATION:
GENERAL INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ILLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11816
LENGTH: 7561
TYPE: DNA
ORGANISM: Human
US-09-949-016-11816
                                                                                                                                        RESULT 13
US-09-949-016-13895/c
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US-09-949-016-11816/c
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; ORGANISM: Human
US-09-949-016-74
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                         Sequence 13895, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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0.27;
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Sequence 29006, Application US/09270767
Patent NO. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29006
LENGTH: 364
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; ORGANISM: Drosophila melanogaster
US-09-270-767-29006
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US-09-270-767-29006
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; ORGANISM: Human
US-09-949-016-13895
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Best Local Similarity 51.2%;
Matches 105; Conservative
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LENGTH: 7562
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Best Local Similarity
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Pred. No. 0.38;
0; Mismatches 96;
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Pred. No. 0.45;
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RESULT 15 US-09-270-767-13109

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Sequence 13109, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13109
LENGTH: 761
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-13109
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Search completed: September 1, Job time: 102.545 secs
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Post-processing: Minimum Match 0%
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AC110299	AC100797	AC114566	AC116502	AC003694	AL592071	AC006177	AC149086	AC140332	RATIGFBP1	AC109570	AC097952	AL442125	AC097039	RATPKRL1	G67173	HUMIGFBPB1	RNLPKG	AX827302	E14395	AR175909	A57715	G67139	AC148834	AC146117	AC146152
AC110299 Homo sapi	AC100797 Homo sapi	AC114566 Mus muscu	AC116502 Mus muscu	AC003694 Mus muscu	AL592071 Human DNA	AC006177 Homo sapi	AC149086 Mus muscu	AC140332 Mus muscu	M89791 Rattus norv	AC109570 Rattus no	AC097952 Rattus no	AL442125 Human DNA	AC097039 Rattus no	M17088 Rat pyruvat	G67173 IGFBP1 5'A	M23592 Human insul	X05684 Rat L-PK ge	AX827302 Sequence	E14395 gDNA encodi	AR175909 Sequence	A57715 Sequence 1	G67139 IGFBP1 X1.1		AC146117 Pan trogl	AC146152 Pan trogl

ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS JOURNAL COMMENT LOCUS DEFINITION RESULT 1 RATILGEZ Ş 망 Ś 밁 Ś ORIGIN FEATURES REFERENCE Best Local Similarity Matches 218; Conservat Query Match source 813 264 144 TGCGCCCATGTCACAAGCAAAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC Unterman,T.G., Lacson,R.G., McGary,E., Whalen,C. and Goswami,R. Biochem. Biophys. Res. Commun. (1991) In press Original source text: Rattus norvegicus (strain Sprague-Dawley) male adult liver DNA. M84484.1 GI:204927 insulin-like growth factor. Rattus norvegicus (Norway rat) Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M84484 RATILGFZ 1181 by Rattus norvegicus insulin-like Rattus. CCAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGG CTGACAATCATTAACCCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAG TGTGCGGAGCTCACAAGCAAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCC (bases 1 to 1181) Conservative /tissue_type="liver" /dev_stage="adult" organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="Sprague-Dawley" 'db_xref="taxon:10116" 'sex="male" ocation/Qualifiers . .1181 57.6%; Score 214.4; DB 10; 97.3%; Pred. No. 1.5e-51; tive 0; Mismatches 6; ď growth DNA A linear ROD 27-facter gene fragment. 6; Indels Length 1181; and Goswami, R.G. ROD 27-APR-1993 <u>.</u> Gaps 323 263 932 203

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                                                     TITLE
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                                                           Allen, C., Allen, H., Alborocks, S., Andin, M., Angulano, C., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Balawin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Balowin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, M., Bhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Canter, D., Davis, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Doyan, R., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, C., Kinley, M., Genter, M., Garcia, A., Garner, T., Garza, M., Ferster, P., Halls, T., Hamilton, K., Harvey, Y., Harles, M., Henderson, M., Hernandez, J., Harvey, Y., Hines, S., Hadun, S. L., Hodgson, M., Hernandez, J., Harvey, Y., Hines, S., Hadun, S. L., Hodgson, M., Hernandez, J., Harvey, Y., Hines, S., Hadun, S. L., Hodgson, M., Hollins, B., Howells, S., Hally, K., S., Hune, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Korat, C., Karpathy, S., Kelly, S., Kenn, Y., Martinez, B., Montenayor, J., Moore, S., Morgan, M., Morris, K., Margum, A., Mangum, A., Mangum, A., Mangum, A., Mangum, M., Marin, R., Martinez, B., Montenayor, J., Moore, S., Morgan, M., Ken, Y., Rose, M., Rose, R., Raiz, S., J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Sherty, J., Shattsbeyn, A., Scott, G., Shatsman, S., Shen, H., Shenty, J., Sherty, J., Shottsbeyn, A., Scott, G., Shere, K., Mang, J., Wang, O., Wang, S., 
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HTG; HTGS_PHASE1.
Rattus norvegicus (Norway rat)
Rat Genome Sequencing Consortium
                                                     Direct Submission
                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                    (bases 1 to 185148)
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Submitted (01-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.ttmc.edu/docs/Genbank draft_data.h
NOTE: This is a 'working draft' sequence. It currently
consists of 63 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
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Center clone name: CH230-97018
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53941: gap of unknown 1
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Lee, U., Greenbaum, L., Haber, B.A., Nagle, D., Lee, V., Miles, V., Mohn, K.L., Bucan, M. and Taub, R. Structure and localization of the IGFBP-1 gene and its expression during liver regeneration
Hepatology 19 (3), 656-665 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1992) R.A. Taub, Univ. of Pennsylvania, Howard Hughes Medical Institute, Clinical Research Bldg., Room 475, 422 Curie Boulevard, Philadelphia, PA 19104-6145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1363)
Mohn,K.L., Waddle,J.R. and Taub,R.
Comparison of mouse and human IGFBP-1 genes reveals a potential
insulin-responsive sequence and conservation of all intron/exon
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Mus musculus (house mouse)
Mus musculus
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3 (bases 1 to 1363)
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                                                                                                                                                                                                                                                                                                                                           /cell line="NIH 3T3"
/cell_type="fibroblast"
/clone_lib="genomic, lamb
/dev stage="embryo"
5n0 - 500
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                                                                                                                                                                                                                        /note="Caat
sequences"
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/product="insulin-like growth factor
/protein_id="CAA47832.1"
/db_xref="GA1:52700"
/db_xref="GOA:P47876"
/db_xref="UniProt/Swiss-Prot:P47876"
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                                                                            source
                                                                                                                                                                                                                                                              AL Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 12, 2002 this sequence version replaced gi:19847866. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                      database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oliver, K.
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                                                                                                                              VECTOR: pBACe3.6.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
/organism="Mus musculus'
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                   Location/Qualifiers
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Pred. No. 4.3e-44;
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BC013345
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouses cDNA segmences
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                        NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                                        Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC013345 Inear ROD Mus musculus insulin-like growth factor binding protein (CDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                                                                                                                                                                                                                                Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGCATGGTCCACTGCCCGGCGAGACACACAAACCCCAGCGAGCATTGAACACTGCACACGG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGACAATCATTAACCCGTGCTGCCGAGCCAGCCCTTCATAAGGCCCTGGGTATGGCCAG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
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                                                                                                                                                                                                                                                                                                                                          (bases 1 to 1569)
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Pred. No. 5.5e-44;
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                                                                                                                                         .nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
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REFERENCE
AUTHORS
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AY560836
                                                                                                                                         SOURCE
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                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                        DEFINITION
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                                                                                                                                                                                                   /ERSION
                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 103; Conserv
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Li,Y., Klimanis,D. and Hallenbeck,J.M.
Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                                                                                                                                               Spermophilus tridecemlineatus protein 1 (IGFBP1) mRNA, comp. AY560836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: 1 Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                       Spermophilus tridecemlineatus (thirteen-lined ground squirrel) Spermophilus tridecemlineatus
                                                                                                                                                                                               AY560836.1 GI:45505308
                                                                                                                                                                                                                                                                         AY560836
                                                                                   Spermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                    CACACGGCCATCTGCCCAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 367
                                                                                                                                                                                                                                                                                                                                                                CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGCAGCCAGCATGCCCCGCGGAGACACACCCCAGCGAGCATTGAACACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="insulin-like growth factor binding protein 1"
/protein_id="AAH13345.1"
/db_xref="GI:15426483"
/db_xref="GI:15426483"
/db_xref="GI:15426483"
/db_xref="MGI:96436"
/translation="MPBFLTVVSWPFLILLSFQIGVAAGAPQPWHCAPCTAERLGLCP
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GGACVPEPAAPATSTLSSSQHEEAKAAVVSADELSESPEMTEEQLLDSFHLMAPSRED
QPILMMAISTYSSMRAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLFN
QPILMMAISTYSSMRAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Igfbp1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Igfbp1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MGC:14075 IMAGE:4161889"
/tlssue type="Liver, normal. 5 m
/clone lib="WCI CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _xref="MGI:96436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98.2; DB 10;
Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                1507 bp mRNA linear eatus insulin-like growth
                                                                                                                                                                                                                                    complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                    cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1569;
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factor binding
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Query Match
Best Local Similarity
Matches 149; Conserv
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                         1500 bp
Sequence 1608 from Patent WO0210453
AX401932
                                                                                                                                                    Patent: WO 0210453-A
                                                                                                                                                                                                 Elashoff, M.R.
                                                                                                                                                                                                                     Mendrick, D.,
                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                         AX401932.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li,Y., Klimanis,D
Direct Submission
                                                                                                                                                                             Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPEVPAAGLWPFLLLLAVQVSTVASSTQPWHCAPCSAEKLALCP PVPSSCPELSRPAGCGCCPMCALPLGARCGVATARYARGLSCRALPGEPRPLHALTRG QGACVPEPAATPTASGLSS IEKEEAKASMVPERVPPESAEMTEEQLLES FHLMASSSED QDALCYPERATETASGLSS IEKEEAKASMVPERVPPESAEMTEEQLLES FHLMASSSED QPILMNAISTYKSMRAREMADIKKWKQPCRRELYKVLERLAKAQQKAGEEIYKFYLPN CNKNGFYHSKQCETSLDGEAELCWCVYPWSGRRIPGSLEIRGDPNCHQYFNVQN"
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/mb.type="unassigned DNA"
/db xref="taxon:10116"
/note="EMBL/GenBank Accession No. NM_013144"
                                                                                                            Location/Qualifiers
                                                                                                                                                                           toxicology
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/protein_id="AAS67029.1
/db_xref="GI:45505309"
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/mol_type="mRNA"
/db_xref="taxon:43179"
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67.1%;
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Rodentia;
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1608 07-FEB-2002;
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RATIGFB
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                                                                          Mohn, K.L., Melby, A.E., Tewari, D.S., Laz, T.M. and Taub, R. The gene encoding rat insulinlike growth factor-binding is rapidly and highly induced in regenerating liver Mol. Cell. Biol. 11 (3), 1393-1401 (1991)
                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                    M58634.1 GI:204732
IGF binding protein-1.
Rattus norvegicus (Norway
                                                                                                                                                                                                                          M58634
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                                            Original
                                                                      91141487
                                                                                                                                                                                                                                    RATIGFB 1500 bp mRNA
Rat IGF binding protein-1 (rIGFBP-1) mR
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Sequence 5 from Patent EP1344834.
AX827271 GI:39837360
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Mammalia; Eutheria;
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                                source text: Rat, cl
Location/Qualifiers
1. .1500
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="unassigned
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
/mol_type="unassigned DNA"
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Rodentia;
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Pred. No. 2.6e-11;
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                                           cDNA to
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No. 2.6e-1
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Sciurognathi; Muridae;
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Murinae;
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mat_peptide
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61
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Sequence 46
AX163782
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                                                                                                                77;
                                                                                                                                                                                                                                                                             gene expression in liver Patent: WO 0138579-A 46
                                                                                                                                                                                                                                                                                                       Gould-Rothberg, B.E., Dipippo, V.A., Ramseh, T.M. and Gerwein, R.W. Method of identifying toxic agents using nsaid-induced differential
                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                              Patent: WO 0138579-A 46 31-MAY-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway
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                                                                         CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTGTGACCAC
CACTICCECTACTATCTA 78
                         CACTTCCGCTACTAGCTA 367
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235. .975
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Pred. No. 2.
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Pred. No. 2.6e-11;
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                                                                                                                ed. No. 2.8e-11;
Mismatches 1;
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RESULT 11 RATIGFBA

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L22979.1 GI:1098472
insulin-like growth factor binding
Rattus norvegicus (Norway rat)
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Original source text: Rattus norvegicus (strain Sprague-I
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Rat insulin-like
                                                                  Similarity
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                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mpefltvvswpflillsfqvrvvagapqpwhcapctaerleccp
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                                                                                                                                                                                                                                                                                        gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                     gene="IGFBP-1"
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join(153. .525,1850.
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| gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Rattus norvegicus"
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                                                                20.5%;
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                                               Score 76.4; DB 10;
Pred. No. 2.8e-11;
0; Mismatches 1;
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriguee, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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2 (bases 1 to 1510)
Director MGC Project.
Direct Submission
Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) Cancer Genomics Office, National Cancer Submitted (02-AUG-2004) Submitted (02-AUG-2004) National Institutes of Health, Mammalian Submitted (02-AUG-2004) National Institutes of Health (02-AUG-2004) National Institutes of Health (02-AUG-2004) National Institutes (02-AU
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                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 184 Row: e Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6981079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 941 Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Submitted (11-APR-2002) Department of Obstetrics and Gynecology,
Submitted (11-Ilinois at Chicago, 820 S. Wood, Chicago, IL 60612,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kim,J.J., Taylor,H.S., Akbas,G.E., Foucher,I., Trembleau,A., Jaffe,R.C., Fazleabas,A.T. and Unterman,T.G. Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells Biol. Reprod. 68 (1), 24-30 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 3886)
Kim, J.J., Jaffe, R.C. and Fazleabas, A.T.
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/gene="IGFBP-1"
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/db_xref="LocusID:25685"
/db_xref="RATMAP:44422"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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3655...>3886
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Pred. No. 1.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contiguous localization of the genes encoding human insulin-like growth factor binding proteins 1 (IGBP1) and 3 (IGBP3) on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M74587.1 GI:184811
insulin-like growth factor binding Homo sapiens (human)
Homo sapiens
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SKALHVTNIKKWKEPCRIEILYRVVESILAKAQETSGEEISKFYLPNCNKNGFYHSRQCE
TSMDGEAGLCWCVYPWNGKRIPGSPEIRGDPNCQMYFNVQN"
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/note="G00-120-075"
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tissue_lib="lambda Charon4A"
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Search completed: September 1, 2005, 03:26:56 Job time: 2321.24 secs

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10.5	10.8	11.3	11.9	11.9	11.9	12.7	12.8	15.9	16.3	16.3	16.6	16.6	16.9	17.3	17.6	18.1
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ALIGNMENTS

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BF236974
LOCUS
                                                                                              ORIGIN
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Query Match
Best Local Similarity
Matches 103; Conser
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                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tlssue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
plate: LLAM9443 row: j column: 02
High quality sequence stop: 581.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1013)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF236974 1013 bp mRNA linear EST 14-NOV-2000 602026605F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4161889 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF236974.1 GI:11150891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                          /lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/note="Organ: lIver; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP_Library."
                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                          db_xref="taxon:10090"
clone="IMAGE:4161889"
                                                                                                                                                                                                                                                                                                                                                                               .1013
                   26.4%;
92.8%;
Score 98.2; DB 2;
Pred. No. 5.9e-17;
0; Mismatches 8;
  8,
                                         Length 1013;
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257 TGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTG 316

Conservative

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Gaps

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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
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BY783538.1
EST.
                                                                                                                                                               92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genom
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY783538 RIKEN full-length enriched, 17.5 days embryc
Mus musculus cDNA clone L930176D05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house Mus musculus
                                                                                                                                                          Similarity 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Waki, K., Shiraki, T.,
TGCCCAGAGAGCTGTGACCACCACTTCCGCTACCTAGCTA 367
                                                                                            ATGGTCCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                                     ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                             /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="L930176D05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
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                                                                                                                                                                                23.6%;
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                                                                                                                                                          Score 87.8; DB 6;
Pred. No. 4.2e-14;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Konno, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA linear EST 23-MAR-2004
1, 17.5 days embryo whole body
                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic
                                                                                                                                                             Gaps
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  RESULT 4
BY771317
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ACCESSION
VERSION
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SOURCE
ORGANISM
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                                                                                                                                                                                                                          Local
                                               329
                                                                                                                                                  269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 331)

(carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Aizawa, K., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Kusakabe, M., Shibata, Y., Yasunishi, A., Kisuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinis, V., Nakagawara, A., Held, W.A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Nakauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Makauchi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Muramatsu, M., Okazaki, Y., Kawai, J., and Hayashizaki, Y. Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
                                                                                               N
                                                                                                                                                                                                    92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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BY794229 RIKEN full-length enriched, 17.5 days embryc
Mus musculus cDNA clone L930292H24 5', mRNA sequence.
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Tel: 81-45-503-9222
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                                                                                                                                                                                                                            Similarity
TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
                                             TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
                                                                                               ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC
                                                                                                                                             ATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                       /tissue type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="L930292H24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
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                                                                                                                                                                                                                          23.6%;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse)
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                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                    Length 331;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                         269 ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACCACGGCCATC
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             AI785818 401 bp mRNA linear EST 02-
ui78h05.y1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, JarTel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY771317
354 bp mRNA linear EST 23-MAR-2)
BY771317 RIKEN full-length enriched, 17.5 days embryo whole body
musculus cDNA clone L930052G15 5', mRNA sequence.
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EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone _____
'ale body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_11b="RIKEN full-length enriched, 17.5 days embryo
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/mol_type="mRNA"
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RESULT 6
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AI196314

480 bp mRNA linest ui71a07.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1887828 5' similar to gb:M59316_rna1 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                   μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_ESTs: ui78h05.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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EST.
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                                                                                                                                                                                                                                                                                   GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
                                                                                                                                                                                                                                                                                                                              TGGTCCACTGCCGGGGGGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                     GCCCAGAGAGCTGTGACCACCACTACTATCTA 98
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). xhoI shoul
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.8; DB 1;
Pred. No. 8.5e-14;
D; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 401;
                                                                                                             EST 14-OCT-1998
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AI530146
706 bp mRNA linear EST 18-MAR-19 u189f09.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HŪMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project Unpublished (1996)
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1 (bases 1 to 480)
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                                                                                                                                                                                                                                                                                  GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
                                                                                                                                                                                                                                                                                                                                   TGGTCCACTGCCCGCGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone_lib="Sugano mouse liver mlia"
//Clone_lib="Sugano mouse liver mlia"
//Clone="Organ: liver; Vector: pwEl8S-FL3; Site 1: DraIII (CACCATGTG); lst Strand cDNA
(CACTGTGTG); Site_2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEL8S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG. XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 86.8; DB 1;
Pred. No. 8.8e-14;
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AI530146
AI530146.1
                               AIO98594 Iinear EST 20-
ue31e07.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone if available and the contact the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                           GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
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//clone_Torgan: liver; Vector: pMELBS-FL3; Site_1: DraIII
//note="Organ: liver; Vector: pMELBS-FL3; Site_1: DraIII
(CACCATGTGTG); Site_2: DraIII (CACCATGTG); lst Strand cDNA
was primed with an oligo(dT) primer
[ATGTGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMELBS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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Pred. No. 9.5e-14;
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EST
Mus musculus
Mus musculus
AI530313
785 bp mRNA linear EST 18-MAR-1: ui91f01.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889785 5' similar to gb.M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 314 60 1000
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M.Mouse EST Project
WashU-HMM Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 765)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:930344
Seq primer: custom primer used
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                         GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
                                                                                                                                                                                                                                                                                                        TEGTTCCACTECCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185.FL3; Site_1: DraIII
(CACTGTGTGT); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sets of the pME185.FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol shoul
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
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/strain="C57BL"
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92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86.8; DB 1; Length 765; Pred. No. 9.7e-14;
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RESULT 10
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     270
                                                                                                                                                                                                                                                                                                          330 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 367
                                                                                                                                                                                                                                                       61
A1529939 799 bp mRNA linear EST 18-MAR-19 u187C99.1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889392 5' similar to gb:m59316 rnal INSULU-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91;
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AI530313.1
EST.
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                          GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                             TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S.FL3; Site_1: DraIII
(CACTGTGTG; Site_2: DraIII (CACAGTGTG); 1st strand cDNA
Was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S.FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhou shoul
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="female"
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92.9%;
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Pred. No. 9.7e-14;
D; Mismatches 7;
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                                                                                                                   EST 18-MAR-1999
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Seq primer:
                                                AGENCOURT 10789306 NIH MGC 152 Mus musculus IMAGE: 6766752 5', mRNA sequence
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                      CA478518
CA478518.1 GI:24936188
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Sugano mouse liver mlia"
//clone lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
/(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst Strand cDNA
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[ATCTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
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vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
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constructed by Dr. Sumio Sugano (University of Tokyo
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sequencing: 5' end primer CTGTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/mol_type="mRNA"
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/clone="IMAGE:1889392"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 86.8; DB 1;
Pred. No. 9.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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AI790802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Al790802 848 bp mRNA linear EST 02-000 bp. MRNA linear EST 02-000 k28b10.y1 Sugano mouse kidney mkia Mus musculus cDNA clore IMAGE:1970299 5' similar to gb:x81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE); mRNA sequence.
Unpublished (1999)
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M. 1 (bases 1 to 848)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., W. Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowerg Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Natter, E., Kohn, S., Band Wilson, M., Natter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Natter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Natter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Natter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Natter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Natter, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; I
(bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                 Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plates: LLWM00138 row: m column: 23 High quality sequence stop: 536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI790802.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Mark Bittinger
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTCCACTGCCGCGGAGACACACACCCGGCGAGCATTGAACACTGCACACGGCCGTCT
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:5338518
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Pred. No. 9.8e-14;
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                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                            Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                                                                                                Bowers, Y
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                                                                                                                                          Schurk, R.,
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RESULT 13
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AI528304
AI528304.1
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852 bp mRNA linear EST 18-MAR-19 ui15910.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1890210 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 852)
                                                                                                                                                                                                                                                                                                                                                       EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:987039
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//Clone_Torgan: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACCATGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTGTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:4442439
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Pred. No. 9.9e-14;
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                                    1 (bases 1 to 605)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ui69d08.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1887663 5' similar to gb:M59316 rna1 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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Location/Qualifiers
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Fax: 314 286 1810
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//note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
//note="Organ: liver; Vector: pME18S-FL3; Ist Strand cDNA
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo (dT) primer
[ATCTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTGTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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Pred. No. 9.9e-14;
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Length 852; Indels

XhoI should

3' end

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Gaps

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329 60

linear

EST 14-OCT-1998

Dubuque, T.

JOURNAL

Unpublished (1996)

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SOURCE
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KEYWORDS
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                                                                                                                                             AUTHORS
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 380)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Schn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                                                                                                                                                                                                                                                                                                                                                          AI785039 380 bp mRNA linear EST 02-
ui73a06.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1888018 5' similar to gb:181579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
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Fax: 314 286 1810
                 Waterston, R. and Wilson, R. The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                               AI785039
AI785039.1 GI:5332755
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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//note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII
/(CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/sex="female"
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/db_xref="taxon
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Pred. No. 2.6e-13;
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61
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Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                  TCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCC 332
CAGAGAGCTGTGACCACCATTGCCACTACTATCTA 95
                                                                                                   TCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                   /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-FL3; Site 1: DraIII
(RACTGTGTG); Site 2: DraIII (CACCATGTG); list Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [GTGTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). KhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="taxon:10090"
'clone="IMAGE:1888018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                     22.1%;
91.6%;
                                                                                                                                                                                                                        Score 82.2; DB 1;
Pred. No. 1.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stop:
                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                               Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contact the
                                                                                                                                                                                                0,
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                                                                                                                                                                                                   Gaps
                                                                                                     60
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Search completed: September 1, 2005, 06:56:52
Job time: 2831.35 secs

0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 2000000000
Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/US10P_PUBCOMB.seq:*
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26: /cgn2_6/ptodata/2/pubpna/US10P_PUBCOMB.seq:*
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372
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                                    / Ggn2 6/ptodata/2/pubpna/US09 PUBCOMB.seq: *
/ Cgn2 6/ptodata/2/pubpna/US10 PUBCOMB.seq: *
/ Cgn2 6/ptodata/2/pubpna/US1 NEW PUB.seq: *
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2248.600 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7	ი 6	5	4	(L)	2	1	Result No.
76.4	154	219	219.4	223.6	321	372	Score
20.5	41.4	58.9	59.0	60.1	86.3		Query Match
1500	423	219	270	423	321	372	Query Match Length DB
9	ø	9	9	9	9	9	
US-09-917-800A-1608	US-09-972-916A-6	US-09-972-916A-2	US-09-972-916A-3	US-09-972-916A-6	US-09-972-916A-4	US-09-972-916A-5	ID
Sequence 1608, Ap	Sequence 6, Appli	2	Sequence 3, Appli	6		ۍ ۲	Description

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٠	•	9.1									9.4		٠	٠	٠	9.6					9.9	10.1			10.2										20.5		
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20	21	19	17								17	13	20	18	10	21			16	17	17	14	16	17	15	17			18	17	22	22				17	,
US-10-719-993-35505	US-10-741-600-17905	US-10-741-601-5746	US-10-227-577-1270	US-10-091-504-1270	US-09-764-869-1270	US-10-227-577-1269	US-10-091-504-1269	US-09-764-869-1269	-10	US-10-011-585A-76	-10	-10	-10-	-10-424-599-6102	-09-918-995-2	-10-	US-10-037-182-3	09-845-583-1	US-10-029-386-5186	-10-094-749-9	1	US-10-017-122-1	US-10-029-386-20306	US-10-221-613-148	US-10-311-455-970	J	-60	916A-1	US-10-152-319A-2150	US-10-388-934-36	US-10-893-315-160	-10-893-	-10-756-149	0	-10-152-319	-10-19	,
35505,	17905,		1270,	æ	1270,	1269,	1269,	1269,	1508	Sequence 76, Appl			Sequence 5461, Ap				ი ი	-	Sequence 5186, Ap		_		Sequence 20306, A			e -	w	1, At	Sequence 2150, Ap	36,		126,	e 1484	2393,	161	Sequence 73, Appl	;

ALIGNMENTS

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US-09-972-916A-5
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                      Query Match 100.0%; Score 372; DB 9; I Best Local Similarity 100.0%; Pred. No. 2.5e-116; Matches 372; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09972916A
Patent No. US20020107198A1
                                                                                                                                                                                                                                                                                      FEATURE:
61 GGCCAGAGTCCAGGAACCACGGGAGTGCCCCCGTGCGCCCATGTACACTGGGGGCCAGAGT 120
                                               ш
                                                                          1 TACACTGGGGGCCAGAGTCCAGGAACCCACGGGAGTGCCCCCGTGCGCCCCATGTACACTGGG
                                               TACACTGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGG 60
                                                                                                                                                                                     Length 372;
                                                                                                                                        Indels
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US-09-972-916A-4
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Patent No. US20020107198A1

GENERAL INFORMATION:
APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
LENGTH: 321
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                          Matches 321;
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                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                     TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGTGCTGCCGAG
                                                                                                                                                                                                                   TACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCCATGTACACTGGG
CTTCCGCTACTAGCTAGCCGC
              CTTCCGCTACTAGCTAGCCGC 372
                                                 CAMACCCAGCGAGCATTGAACACTGCACACGCCATCTGCCCAGAGAGCTGTGACCACCA
                                                                         CAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCACCA 351
                                                                                                  CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                          CCAGCCCTTCATAAGGCCCTGGGTATGGCCAGCCAGCATGGTCCACTGCCCGCCGAGACA
                                                                                                                                                   TATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGTGCTGCCGAG
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                                                                                                                                                                                                                                                                                                      86.3%; Score 321; DB 9; I ilarity 100.0%; Pred. No. 5.8e-99; Conservative 0; Mismatches 0;
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321
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US-09-972-916A-6
Sequence 3, Application US/09972916A
Patent NO. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/99/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR PILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 30
SEQ ID NOS: 6
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LENGTH: 423
TYPE: DNA
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Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 GCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGGGCCAGAGTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 ACTOTGGCCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCC
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76.2%;
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Pred. No. 9.6e-66;
0; Mismatches 74
                                                                                                                                                                                                                                                                                           423
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TYPE: DNA ORGANISM: Artificial Sequence

FEATURE:

LENGTH: 270

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US-09-972-916A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
APPLICANT: Thule, Seter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
                                     Sequence 6, Application US/09972916A Patent No. US20020107198A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09972916A Patent No. US20020107198A1
                                                                                                                                                                                                                                                                                                                                                                          Matches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 220; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE
FILE REFERENCE: US 1292/01 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                      334
                                                                                                                                                                                                    121
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                                                                                                                                                                       AGAGAGCTGTGACCACCACTTCCGCTACTAGCTAGCCGC 372
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             SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                         Score 219; DB 9; pred. No. 3e-64; 0; Mismatches
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Pred. No. 2.3e-64;
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US-09-917-800A-1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR PPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR APPLICATION NUMBER: US 60/290,045
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-07
PRIOR PILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-07-09
                                                                                                                  SOFTWARE: PatentIn Ver.
SEQ ID NO 1608
LENGTH: 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1608, Application US/09917800A Patent No. US20020119462A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.4%; Score 154; DB 9; Best Local Similarity 100.0%; Pred. No. 5e-42;
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APPLICANT: Porter, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
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APPLICANT:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                  OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_013144
                                            ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CCAGGAACCACGGGAGTGCCCCGTGCGCCCATGT 154
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Castle, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porter, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elashoff, Michael
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APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotaxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
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US-10-388-934-5
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Best Local Similarity
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Publication No. US20040005547A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
-10-388-934-5
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APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
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CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
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APPLICANT: Wolf, De
TITLE OF INVENTION:
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No. US20040014040A1
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98.7%;
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Pred. No. 1.9e-15;
0; Mismatches 1;
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; OTHER INFORMATION: Genbank Accession No. NM_013144 US-10-152-319A-1613
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; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_013144
US-10-191-803-73
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PRIOR FILING DATE: 2001-06-13
PRIOR PELICATION NUMBER: US 60/298,925
PRIOR PELING DATE: 2001-06-19
PRIOR PELING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR PELING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
                                                                                                                                                                                                Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1613
LENGTH: 1500
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Publication No. US20040072160A1
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 73
    Matches
                                             Query Match
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Matches 77; Conserv
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
                                                                                                                                TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
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ORGANISM: Rattus norvegicus
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  Local Similarity 98.
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Score 76.4; DB 18; Length 1500;
Pred. No. 1.9e-15;
0; Mismatches 1; Indels 0;
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Pred. No. 1.
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APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-W0

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR APPLICATION NUMBER: US 60/237,054
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US-10-756-149-1484
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US-09-880-107-2393
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Sequence 1484, Application US/10756149

Publication No. US20050181375A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert

TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS;

TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

FILE REFERENCE: file

CURRENT APPLICATION NUMBER: US/10/756,149

CURRENT FILING DATE: 2004-01-12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                676
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RESULT 13
US-10-893-315-126
Sequence 126, Application US/10893315
Sequence 126, Application US/10893315
Publication No. US20050147987A1
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 217-2
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 126
SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                         US-10-893-315-126
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; ORGANISM: Homo
US-10-756-149-1484
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                   Query Match
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SEQ ID NO 1484
LENGTH: 6128
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9173
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                 1842 TCCTCCCACCAGCGGTTTGCGTAGGGCCTTGGGTGCACTAGCAAAACTTATTTTGA 1901
                                                                                                                                                                                                                                                                                                156;
                                                                                                                                                                 180 ACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCC------GTGCTGCCG 229
                                                                                                                                                                                                                                        120 TCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTCACAAAGCAAACCAAACTTATTTTGA 179
290 CACAAACCCAGCGAGCATTGAACACTGC-ACACGGCCATCTGCCCAGAGAGAGCTGTGACCA 348
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63.2%;
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Pred. No. 5.7e-11;
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Pred. No. 5.2e-11;
0; Mismatches 72
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CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 36
                                                                                                                                                                                                                                                                                      RESULT 15
US-10-388-934-36/c
US-10-388-934-36/c
; Sequence 36, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
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SEQ ID NO 160
LENGTH: 9174
TYPE: DNA
ORGANISM: Human
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Publication No. US20050147987A1
GENERAL INFORMATION:
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Best Local Similarity 63.2
Matches 156; Conservative
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION.
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
                                                                                                                                                                                       TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY FILE REFERENCE: 21199
                                                                                                                                                                                                                           APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
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PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                          ; LENGTH: 13011
TYPE: DNA
ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-36
                                                                                                          Query Match
Best Local Similarity
Matches 60; Conserv
3028 CGCCCATG 3021
                                                       3088 TGCCAACGGAAGCCTTGTACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCCTG 3029
                                                                        35 TGCCCCGTGCGCCCATGTACACTGGGGGGCCAGAGTCCAGGGAACCACGGGAGTGCCCCGTG 94
                           95 CGCCCATG 102
                                                                                                                    Conservative
                                                                                                                              14.8%;
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                                                                                                                Score 55.2; DB 17;
Pred. No. 5.3e-08;
0; Mismatches 8;
                                                                                                                                              DB 17;
                                                                                                                                              Length 13011;
                                                                                                                    Indels
                                                                                                                  0;
                                                                                                                    Gaps
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Search completed: September Job time: 1085.43 secs ۲, 2005, 16:44:30

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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    seq
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length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Match Length
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   1202784 seqs, 818138359 residues
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                   9173
9174
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3 US-08-945-140-1

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US-09-949-016-11786

US-09-949-016-12957

US-09-949-016-12957

US-09-949-016-12957

US-09-949-016-1214710

US-09-949-016-121471

US-09-949-016-121471

US-09-949-016-121471

US-09-949-016-121471

US-09-949-016-121471

US-09-949-016-121471

US-09-949-016-12153

US-09-949-016-12153

US-09-949-016-12208

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US-09-949-016-12550

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US-09-949-016-177807

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US-09-949-016-177807

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US-09-949-016-177807

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US-09-277-767-31109
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 30, Appl
36, Appl
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1796, A
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CCACTTC	AGCC CCTG CACA	ACAC	TCCA	2.8 8.8 2.6 8.8 2.6 8.8 2.6 8.8 2.2 8.7 2.2 8.7 2.3 8.6 2.4 8.5 2.5 8.5 2.6 8.5 2.7 8.7 2.7
TTC 3	AGCCC HGCCC	CCCAC GGGGA TCAGC	Similarity 6; Conserva TCCAGGAACCA	2.8 8.8 8.8 2.6 8.8 8.8 2.6 8.8 8.8 8.8 2.6 8.8 8.7 2.2 8.7 2.2 8.7 2.2 2.8 8.7 2.2 2.2 8.7 2.2 2.2 8.7 2.2 2.3 8.6 3.3 2.6 8.6 3.3 2.6 8.5 3.
:CAGCGAG 355 2080	TTCATA	CAGCGG	17. 63. vative	32.8 8.8 2130 4 US-09 32.6 8.8 907 4 US-09 32.6 8.8 134008 4 US-09 32.2 8.7 505 4 US-09 32.2 8.7 601 4 US-09 32.2 8.7 23847 4 US-09 32.2 8.7 23847 4 US-09 32.2 8.7 4447 3 US-08 32.2 8.7 4447 3 US-09 32.2 8.7 4343 4 US-09 32.8 8.5 2194 4 US-09 31.6 8.5 2194 4 US-09 31.6 8.5 1348 4 US-09 31.6 8.7 4447 2 US-09 32.2 8.7 4444 4 US-09 32.2 8.7 4444 4 US-09 32.2 8.7 4444 4 US-09 32.2 8.7 444 4 US-09 32.2 8.7 4444 4 US-09 32.2 8.7 4444 4 US-09 32.2 8.7 444 4 US-09 32.2 8.7 444 4 US-09 32.2 8.7 4444 4 US-09 32.2 8
CATC	AGGC AGGT	CACG	2*; 2*; 2*;	
CATCCAGCGAGCATCTGCCGCCGCCGCCGCCACCCTCCCAGAGAGCACTGGCCATTC 355	AGCCAGCCCTTCATAAAGGCCCTGGGTATGGCCAGCCAGC	TCCTCCACCAGCGGTTTGCGTAGGGCCTTGGGTGCACTAGCAAAACAAAC	17.2%; Score 63.8; DB 4; Length 9173; imilarity 63.2%; Pred. No. 2.2e-10; Conservative 0; Mismatches 72; Indels 19; Gaps TCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTCACAAGCAAACTTATTTGA	-909-962A-6 -909-962A-7 -909-962A-7 -909-962A-7 -909-962A-7 -909-962A-7 -909-962A-7 -909-962A-8 -909-962-96-15639 -909-962-96-15639 -909-962-30 -909-9
CCAGAGAGCACTGGCCA 2073	GAGA	NAACAAACTTATTTTGA 1901GTGCTGCCG 229 TGGTGCAAGTGGCGCGG 1961	٠ س	Sequence 6, Appli Sequence 7, Appli Sequence 65, Appl Sequence 13841, A Sequence 15639, A Sequence 177808, Sequence 177809, Sequence 3669, Ap Sequence 3, Appli Sequence 1177, Ap Sequence 1177, Ap Sequence 11745, A Sequence 16824, A Sequence 16824, A Sequence 16824, A Sequence 16824, A Sequence 10411, A Sequence 10411, A Sequence 404, App

RESULT 2 US-09-949-001-36 ; Sequence 36, Application US/09949001 ; Patent No. 6825336

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TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR APPLICATION NUMBER: 60/231,323
PRIOR TILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: ^~-
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Best Local Similarity
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ORGANISM: Human
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 9174
             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMER: FR 95/04558
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                             NERAL INFORMATION:

APPLICANT: CHEN, Ruihuan

APPLICANT: DOIRON, Bruno

APPLICANT: KAHN, Axel
                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 19426
                                                                                           FILING DATE:
                                                                                                          APPLICATION NUMBER:
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Collegeville
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                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791
FILING DATE: January 30, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Makoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Makoto MURASE et al.
TITLE OF INVENTION: Method for Increasing Storage
TITLE OF INVENTION: Lipid Content in Plant Seed
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 194 base pairs
TYPE: nucleic acid
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FILING DATE: 12-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: EX950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
               LENGTH: 13011 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 805 Fifte CITY: Washington
                                                                                                               TELEX:
                                                                                                                                 TELEFAX:
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 ropology:
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5. 5914449
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linear
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Pred. No. 2.6e-08;
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RESULT 6
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US-09-949-016-11786
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US-09-949-016-11786/c
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                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11786
                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

COMMENTED TO SEC 10 NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                 LENGTH: 15108
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LOCATION:
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                                                                    G 2357
                                                                                                       G 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(3219..3765, 3949..5916, 6009..6151,
6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910,
9480..10162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(3212..3218, 3766..3948, 5917..6008,
6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..807.
9298..9479, 10163..10269)
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6152..6283, 6418..6604, 6921..7191, 7302..7452,
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Pred. No. 0.015;
0; Mismatches 13;
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Pred. No. 1.7e-07
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Sequence 17205, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

FRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

PRIOR PRIOR FILING DATE: 2000-09-08

PRIOR PRIOR FILING DATE: 2000-09-08

PRIOR PRIOR FILING DATE: 2000-09-08

PRI
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APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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; SEQ ID NO 138
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-484-970B-138/c
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; ORGANISM: Human
US-09-949-016-17205
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                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                  Query Match
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 336987.1CB1
                                                                                                                                                                                                                                                     Local Similarity
nes 57; Conserva
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                                                            62 GCCAGAGTCCAGGAACCACGGGAGTGCCCCG 92
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Pred. No. 0.11;
0; Mismatches 34;
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Pred. No. 0.015;
D; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                  Length 3054;
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US-09-949-016-12957/c

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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES :
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-00
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-09
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(35471)
OTHER INFORMATION: n = A,T,C or
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ACTGTGGGGACACCTCGCCTGCACCTCCCTCCCCCAGCCCCGAGCACTGTGGGG
                                                          ACACTGGGGGCCAGAGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGCGCGGACTCCCCCAGGCACACAGCTCCCCAGGGACCAGGGACCAGGGG 22784
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                                                                                                                                   Conservative
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                                                                                                                                Score 36; DB 4
Pred. No. 0.56;
0; Mismatches
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US-09-949-016-14710
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                                                                                                                     Sequence 14710, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER DE SECTION NOW.
                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14710
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PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 18
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CURRENT APPLICATION NUMBER: US/09/845,583A
CURRENT FILING DATE: 2001-04-30
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APPLICANT: Brunken, William Joseph
APPLICANT: Champliaud, Marie-France
APPLICANT: Hunter, Dale
TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Mus musculus
ORGANISM: Human
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Pred. No. 0.36;
0; Mismatches 67;
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RESULT 13
US-09-949-016-12147/c
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US-09-949-016-15394
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US-09-949-016-15394
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Sequence 12147, Application US/09949016
PACENT NO. 6812339
GEMERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 15394
LENGTH: 16520
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: FOLLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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Pred. No. 0.43;
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OF DETECTION AND USES THEREOF
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 17361
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                                                                   Matches
                                                                                                    Query Match
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Best Local (
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TYPE: DNA
ORGANISM: Human
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(767677)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
FEATURE:
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FEATURE:

FEATURE:

LOCATION: (1)...(767677)

OTHER INFORMATION: n = A,T,C
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Local Similarity 51.9%;
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Pred. No. 2.8;
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AGTCCAGGAACCACGGGAGTGCCCCGTGCGCCCATGTACACTGGGGGCCAGAGTCCAGGA 126

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RESULT 15

US-09-949-016-19194/c

Sequence 19194, Application US/09949016

Patent No. 6812239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 19194

LENGTH: 601

TYPE: DNA

ORGANISM: Human

US-09-949-016-19194
Search completed: September 1, 2005, 07:07:16 Job time: 123.652 secs
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Score
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Gapop 10.0 , Gapext 1.0
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AX401932 Sequence
AX827271 Sequence
MS8634 Rat IGF bin
AX163782 Sequence
L22979 Rat insulin
BC078889 Rattus no
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G67139 IGFBP1 X1.1
AX409747 Sequence
M74587 Human insul
G1994 BWSS752 Eri
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AL607124 Mouse DNA
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AL592071	HUMIGFBPB1	AP001752	AC020709	AP001052	AL589702	BV006814	AL442125	AC110517	AC114566	AC116502	AC100797	AC133528	AC110299	RNLPKG	AX827302	E14395	AR175909	A57715	AC109570	AC097952	AF429315	AC148834	AC146117	AC146152	AC091524
AL592071 Human DNA	M23592 Human insul		Homo	AP001052 Homo sapi	AL589702 Human DNA	BV006814 STS CEB24	AL442125 Human DNA	AC110517 Mus muscu	AC114566 Mus muscu	AC116502 Mus muscu	AC100797 Homo sapi	AC133528 Homo sapi	AC110299 Homo sapi	X05684 Rat L-PK ge	AX827302 Sequence	E14395 gDNA encodi	AR175909 Sequence	A57715 Sequence 1	AC109570 Rattus no	Rattu	AF429315 Homo sapi	AC148834 Pan trogl		AC146152 Pan trogl	AC091524 Homo sapi

ALIGNMENTS

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VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
ACCESSION
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AUTHORS
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COMMENT
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325 CCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
                                                                                                                                               205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M84484.1 GI:204927
insulin-like growth factor.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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ilarity 99.5%;
Conservative
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1. .1181
                                                                                                                                                                                                                                                    /tissue_type="liver"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                       sex="male"
                                                                                                                                                                           Score 212.4; DB 1
Pred. No. 1.2e-48;
0; Mismatches 1
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facter gene fragment.
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                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                 Bryant, N. Blay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasas, H., Center, A., Chan, S., Chen, S., Chen, Z., Chu, J., Chandas, V., Carter, K., Cavazos, I., Ceasas, H., Center, A., Chen, Z., Che
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Aldams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anglebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Bena Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
                                                                               Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1
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Genome Sequencing Consortium
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norvegicus clone CH230-97018,
3 unordered pieces.
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B, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Center clone name: CH230-97018
Center clone name: CH230-97018
Cequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 135613 bases at least Q40
Consensus quality: 146849 bases at least Q30
Consensus quality: 145680 bases at least Q20
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Mohn,K.L., Waddle,J.R. and Taub,R.
Comparison of mouse and human IGFBP-1 genes reveals a potential
insulin-responsive sequence and conservation of all intron/exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee,J., Greenbaum,L., Haber,B.A., Nagle,D., Lee,V., Miles,V., Mohn,K.L., Bucan,M. and Taub,R. Structure and localization of the IGFBP-1 gene and its expression during liver regeneration Hepatology 19 (3), 656-665 (1994) 94164648
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/codon_start=1
/product="insulin-like growth factor
/protein_id="CAA47832.1"
/db_xref="GOA:P47876"
/db_xref="GOA:P47876"
                                                                                               964. .>1336
                                                                                                                                                                                                sequences"
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/strain="NIH Swiss"
/db_xref="taxon:10090"
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/cell_type="fibroblast"
/clone_lib="genomic, lan
/dev stage="embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                         source
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                                                                                                                                                                                                                                                humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 12, 2002 this sequence version replaced gi:19847866.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
AL607124
AL607124.15
                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20C9 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                         database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oliver, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG
Mus
                                                                                                                        VECTOR: pBACe3.6.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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PVPASCPEISRPAGCGCCPTCALPMGAACGVATARCAQGLSCRALPGEPRPLHALTRG
QGASLPEPAAPATSTLFSSQHE"
/organism="Mus musculus
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                             Location/Qualifiers
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Pred. No. 6.1e-42
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BC013345
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VERSION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsiah, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, M.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Sakalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences
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                                                                                                                                                                                  Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                          NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC013345 Insulin-like growth factor binding protein (CDNA clone MGC:14075 IMAGE:4161889), complete cds.
                                                                                                                                                                                                                                                                                                  Strausberg,R
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BC013345.1
                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci.
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Pred. No. 5.7e-42;
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ACCESSION
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AY560836
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
Li,Y., Klimanis,D. and Hallenbeck,J.M. Cloning and characterization of insulin-like growth factor binding protein 1 (IGFBP-1) from thirteen-lined ground squirrel
                                                                                             Spermophilus tridecemlineatus (thirteen-lined ground squirrel)
Spermophilus tridecemlineatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurin
                                                                                                                                                                                                               1507 bp Spermophilus tridecemlineatus ir protein 1 (IGFBP1) mRNA, complet AY560336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                             Spermophilus.
                                                                                                                                                                                             AY560836.1 GI:45505308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 92.8
03; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       CACACGGCCATCTGCCCAGAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCCAGCCAGGGATGGTCCACTGCCCGCGAGACACAAACCCCAGCGAGCATTGAACACTG
                                                                                                                                                                                                                                                                                                                                                                CACACGGCCGTCTGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGCAGCCAGCATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTG
                                                              (bases 1 to 1507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="LocusID:16006"
/db_xref="McI:96436"
/db_xref="McI:96436"
/translation="MpeFLTTVVSWPFLILLSFQIGVAAGAPQFWHCAPCTAERLGLCP
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PVPASCPEISRPAGGGCPTCALPMGAAGVATARCAQGLSCRALPGEPRPLHALTRG
GGACVPEPAAPATSTLSSSQHEEAKAAVVSADELSESPEMTEEQILDSFHLMAFSRED
QPILWNAISTYSSMRAREIADLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="insulin-like growth factor binding /protein_id="AAH13345.1" /db xref="GI:15426483" /db xref="GI:15426483"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Igfbp1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: IGFBP-1"
/db_xref="LocusID:16006"
/db_xref="MGI:96436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Liver, normal.
/clone_Tib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="MGC:14075 IMAGE:4161889"
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Pred. No. 1.2e-16;
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                                                                                           Craniata; Vertebrata; Eut
Sciurognathi; Sciuridae;
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Query Match
Best Local Similarity
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Eukaryota; Metazoa; Chordata;
Mammmalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1608 from Patent WO0210453.
AX401932
AX401932.1 GI:21338112
                                                                                                                                                                                              Mendrick,D.,
Elashoff,M.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-FEB-2004) StrokeBranch, NINDS/NIH, Bethesda, MD 20892, USA
                                                                                                                                                   Molecular toxicology modeling Patent: WO 0210453-A 1608 07-FEB-2002,
                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                              Gene Logic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAGCTGCCCAGAGAGCATTGACCACCTGTCC
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Y., Klimanis, D. and Hallenbeck, J.M
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                  /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
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/product="insulin-like growth factor binding
/protein_id="AAS67029"."
/db_xref="GI:45505309"
/db_xref="GI:45505309"
                                                                                                       ocation/Qualifiers
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'note="EMBL/GenBank Accession No. NM_013144"
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organism="Spermophilus"
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67.6%;
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Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                                 83
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                                                                                                                                            Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methods
Patent:
F. HOFFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX827271
Sequence 5:
AX827271
                                                                   1 (bases 1 to 1500)

Mohn, K.L., Melby, A.B., Tewari, D.S., Laz, T.M. and Taub, R. The gene encoding rat insulinlike growth factor-binding is rapidly and highly induced in regenerating liver mol. Cell. Biol. 11 (3), 1393-1401 (1991)
                                                                                                                                                                                                                                                                                                                                                                  8
                                    Original
                                                                                                                                                                                      M58634.1 GI:204732
IGF binding protein-1.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                           M58634
                                                                                                                                                                                                                                      RATIGFB 1500 bp mRNA
Rat IGF binding protein-1 (rIGFBP-1) mR
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                                                                                                                                      Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                  CACAAACCCAGCGAGCATTGAACACTGCACACGCCATCTGCCCAGAGAGCTGTGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ess, F., Suter-Dick, L. and Wolf, D. thods for the toxicity prediction of tent: EP 134884-A 5 17-SEP-2003; HOFFMANN-LA ROCHE AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                    source text:
                    source text: Rat, cl
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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from Patent EP1344834.
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98.7%;
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98.7%;
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Rodentia;
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Pred. No. 1.5e-10;
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                                    cDNA to
                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
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ORGANISM
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VERSION
KEYWORDS
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AX163782
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Best Local Similarity
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mat_peptide
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61
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                                                                                                                                                                                                                                                                                      Gould-Rothberg, B.E., Dipippo, V.A., Ramseh, T.M. and Gerwein, R.W. Method of identifying toxic agents using nsaid-induced differential gene expression in liver patent: WO 0138579-A 46 31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46
AX163782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                      Patent: WO 0138579-A 46 31-MAY-2001;
Curagen Corporation (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AX163782
                                                                                                                                    Similarity
CACTICCGCTACTATCTA 78
                  CACTTCCGCTACTAGCTA 418
                                                          CACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTGTGACCAC
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                                                                                                                     18.1%;
nilarity 98.7%;
Conservative
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235. .975
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                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10116"
/tissue_type="regenerating liver"
/dev_stage="adult"
160._.978
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/protein_id="AAA41380.
/db_xref="GI:204733"
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/strain="Fisher"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:14544878
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98.7%;
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                                                                                                                     Score 76.4; DB 6;
Pred. No. 1.5e-10;
0; Mismatches 1
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Pred. No. 1.5e-10;
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RESULT 11 RATIGFBA

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MEDLINE
                                                             Query Match
Best Local
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On Nov 30, 1995 this sequence version replaced gi:385167.
Original source text: Rattus norvegicus (strain Sprague-I
DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lacson, R., Oehler, D., Yang, E., Goswami, R. and Unterman, T. Dideoxy sequencing and structural analysis of the rat ins growth factor binding protein-1 gene Biochim. Biophys. Acta 1218 (1), 95-98 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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L22979
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                                                                Similarity
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="IGFBP-1"
join(153. .525,1850. .
/gene="IGFBP-1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                         PVPASCPEISRPAGCGCCPTCALPLGAACGVATAACAQGLSCRALPGEPRPLHALTRG
QGACVLEPAAPATSSLSGSQHEEAKAAVASEDELAESPEMTEEQLLDSFHLMAPSRED
QPILMNAISTYSSMRAREITDLKKWKEPCQRELYKVLERLAAAQQKAGDEIYKFYLPN
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                                                                                                                                                                                                                                                                                 /gene="IGFBP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="insulin-like growth factor binding
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/db_xref="GI:1098473"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="liver"
/dev_stage="adult"
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/db_xref="taxon:10116"
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                                                                                                                                                                        number=3
                                                                                                                                                                                      9003. .4089
gene="IGFBP-1"
                                                                                                                                                                                                                                    gene="IGFBP-1"
                                                                                                                                                                                                                                                                    number=2
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                                                                                                                                                                                                                                                                                                                                                               'number=1
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98.7%;
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                                              Score 76.4; DB 10;
Pred. No. 1.5e-10;
0; Mismatches 1;
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RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 CACTTCCGCTACTAGCTA 418
                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: e Column: 23
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing Sy: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                       passed the following selection criteria: matched mRNA gi: 6981079
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Direct Submission
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broc. Natl. Acad. Sci. U.S.A. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.
Dickson, M., Schmutz, J., Grimwood, J., Rodri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RATTUS norvegicus insulin-like growth factor binding protein 1, mRNA (cDNA clone MGC:93595 IMAGE:7129185), complete cds.
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/organism="Rattus norvegicus"
/mol_type="mRNA"
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Rodentia; Sciurognathi; Muridae;
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Best Local Similarity
Matches 66; Conserv
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                                                                                                                            Kim,J.J., Jaffe,R.C. and Fazleabas,A.T.
Direct Submission
Submitted (11-APR-2002) Department of Obstetrics and Gynecology,
University of Illinois at Chicago, 820 S. Wood, Chicago, IL 60612,
                                                                                                                                                                                                                               Kim, J.J., Taylor, H.S., Akbas, G.E., Foucher, I., Trembleau, A., Jaffe, R.C., Fazleabas, A.T. and Unterman, T.G. Regulation of insulin-like growth factor binding protein-1 promoter activity by FKHR and HOXA10 in primate endometrial cells Biol. Reprod. 68 (1), 24-30 (2003)
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                                                                                                                                                                                                                                                                                                                                                     Papio anubis (olive baboon)
Papio anubis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY095345

Papio anubis insulin-like growth factor binding protein-1 (IGFBP-1)
                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Papio.
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                            /organism="Papio anubis
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142...960
/gene="IGFBP-1"
                                                                                                    Location/Qualifiers
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/lab_host="DH10B"
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316 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGC 375
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                                                                 Buffer:
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IGFBP1 X1.1 Human Homo
G67139
G67139.1 GI:10186730
                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 448)
Cox,D.G., Boillot,C. and Canzian,F.
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                              STS size: 448
                                                                                                                                                                                                                                                       Fax: +33-4-72738388
                                                                                                                                                                                                                                                                                                                  Genome Analysis Group
                                                                                                                                                                                                                                                                                                                               Contact: Federico Canzian
                                                                                                                                                                                                                                                                                                                                                                           Genome Survey
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A: TGCACTAGCAAAACAA
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/product="insulin-like
3655. .>3886
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                                                                                              Vol:
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9 8 9 B	Matches Oy Db	RESULT 15 AX409747 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES BOUICE ORIGIN ORIGIN	STS STS Prime Prime ORIGIN Query Ma Best Loc Matches Qy Db Qy Db Db
533 TAACCTCCTGGTGCAAGTGGCGCGGCCTTTATAAGGTGCGCGCTTGTCCAGC 316 CAGCATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGC-ACACGG	ches 141 206 473 266	AX409747 AX409747 Sequence 2394 from Patent WO0229103. AX409747.1 GI:21442452 . Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, Gene expression profiles in liver cancer Patent: WO 0229103-A 2394 11-APR-2002; Gene Expression Profiles in liver cancer Patent: WO 0229103-A 2394 11-APR-2002; GENE LOGIC INC (US) 16128 /organisms="Homo sapiens" /mol_type="unassigned DNA" /mol_type="unassigned DNA" /note="EMBL/GenBank Accession No. M74587" /note="EMBL/GenBank Accession No. M74587"	## Coation/Qualifiers 1448 1448
GTGTCAGC 592 GC-ACACGG 374 H H H GCGCCGCCG 644	19; Gaps 3; "IGACAATCAT 265 "IGCCAATCAT 532 "TATGGCCAGC 315	PAT 14-JUN-2002 Buteleostomi; Homo. J.G.	3; 19; GADS 3; 19; GADS 3; 19

Db 645 CCACCCTCCCAGAGAGCACTGGCCACCGCTCC 676

Search completed: September 1, 2005, 03:27:00 Job time: 2637.79 secs

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Result
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10.8	10.9	11.2	11.2	11.5	11.5	11.9	12.7	12.7	12.7	13.0	13.2	13.9	14.4	14.4	14.6	14.6	14.8	15.2	15.5	15.9
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Query Match 23.2%; Score 98.2; DB 2; Length 1013; Best Local Similarity 92.8%; Pred. No. 3.7e-17; Matches 103; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	/organism='Mus musculus" /mol_type="manka" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4161889" /lab host="DH108 (Tl phage-resistant)" /lab host="DH108 (Tl phage-resistant)" /clone_lib="NCI CGAP_Li9" /clone="Organ: liver; Vector: pCMV-SPORT6; Site_l: NotI; /note="Organ: liver; Vector: pCMV-SPORT6; Site_l: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Site_2: SalI; cloned unidirectionally. Tife Technologies. Note: this is a NCI_CGAP Library."	Contact: Gentact: Gentact: Gentact: Gentact: Gentact: Color Libb CDNA Libb CDNA Libb CDNA Seque Clone ditfound throughttp://imarticher: LL! High quali	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6B), 1273-1289 (2003)
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TGCCCAGAGAGCTGTGACCACCTTCCGCTACCTAGCTA 418
                                                                                          ATGGTCCACTGCCCGCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATC 379
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                                                                                                                                                                                                                                                                              /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/clone="L930176D05"
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                                                                                                                                                                                                                        Local
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62 TGCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 100
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                                                                                               N
                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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BY794229 RIKEN full-length enriched, 17.5 days embryc
Mus musculus cDNA clone L930292H24 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further details.
                                                                                                                                                                                                                        Similarity
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                                                                                                                                 ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC
                                                 TGCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 418
                                                                                               ATGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTC 61
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                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                             /tissue type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                       clone="L930292H24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    db xref="taxon:10090"
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                                                                                                                                                                                               Score 87.8; DB 6;
Pred. No. 2.8e-14;
D; Mismatches 7
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Sciurognathi;
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1, 17.5 days embryo whole body
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thi; Muridae; Murinae; Mus
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Best Local
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                                                                                                                                                                                                                                                                                                        320 ATGGTCCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATC 379
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A1785818
401 bp mRNA linear ui78h05.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1888569 5' similar to gb:X81579 M.musculus mRNA for them: "nen'lin-like growth factor binding (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                   92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Alzawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aldinis, V., Nakagawara, A., Held, W., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Makauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramateu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y. Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia Genome Res. 13 (6B), 1273-1289 (2003)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prepare mouse tissues.
Please visit our web
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/mol_type="mRNA"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="L930052G15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
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EN full-length enriched, 17.5 days embryo whole body
cDNA clone L930052G15 5', mRNA sequence.
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No. 2.8e-14;
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AUTHORS
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91;
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The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTs: ui78h05.x1
Contact: Marra M/WashU-NCI Mouse EST project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                 TGGTCCACTGCCCGCCGAGACACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT 380
                                                                                                                                                                                                                                               GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                                                TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pMEL8S-FL3; Site_1: DraIII
/note="Organ: liver; Vector: pMEL8S-FL3; Site_1: DraIII
(CACCAGTGTG); Site_2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEL8S-FL3
vector [5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Traffirite of Medical Science). Custom primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute of Medical Science). Custom primers sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.8; DB 1;
Pred. No. 5.7e-14;
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AIS30146 706 bp mRNA linear EST 18-MAR-19 u189f09.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1889609 5' similar to gb:M59316 rnal INSULI-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 480)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubi
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGTCCACTGCCCGCGGAGACACACACCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Sugano mouse liver mlia" // note="Organ: liver; Vector: pME18S-FL3; Site 1: DrallI (CACTGTGTG); Site 2: DrallI (CACTGTGTG); Ste 5trand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DrallI adaptor [TGTTGGCTACTGG], digested and cloned into distinct DrallI sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shou be used to isolate the CDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACACA."
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/lab_host="DH10B"
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Pred. No. 5.9e-14;
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                                                                                                                                                                                                                                                                            381 GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 418
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AI098594 "MAXIN THE MIS MUSCULUS CDNA CLONE UE31e07.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1481988 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 706)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., The Washu-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                             GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA 98
                                                                                                                                                                                                                                                                                                                             TGGTCCACTGCCCGCGGAGACACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Glone liber Sugano mouse liver mlia"
/Glone liber Sugano mouse liver mMIAS.-FL3; Site 1: DraIII
/noter Torgan: liver; Vector: pMEIAS.-FL3; Site 1: DraIII
(CACCATGTG); Site 2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTTT]; double stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pMEIAS-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shou
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACAA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      performed to exclude fragments <1.5kb.
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:1889609"
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/strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86.8; DB 1;
Pred. No. 6.4e-14;
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RESULT 9
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Best Local (
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuk Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI098594.1 GI:3448119
EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:930344
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                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                 GCCCAGAGAGCTGTGACCACCATTGCCACTACTATCTA
                                                                                                                                                                                                                                      GCCCAGAGAGCTGTGACCACCACTTCCGCTACTAGCTA 418
                                                                                                                                                                                                                                                                                 TGGTCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCACACGGCCGTCT
                                                                                                                                                                                                                                                                                                                       TGGTCCACTGCCCGCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DrallI
(CACTGTGTG); Site_2: DrallI (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DrallI adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DrallI sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 86.8; DB 1
Pred. No. 6.5e-14
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1st strand cDNA
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RESULT 10
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AI529939 799 bp mRNA linear EST 18-MAR-19 ui87c09, y1 Sugano mouse liver mlia Mus musculus CDNA Clone IMAGE:1889392 5' similar to gb:#859316 rnal INSULU-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:#81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                91;
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The WashU-NCI Mouse EST Project 1999
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/note="Organ: liver; Vector: pME18S.FL3; Site 1: DraIII (CACCATGTG); lst Strand cDNA (CACCATGTG); lst Strand cDNA was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S.FL3 vector (5' site CACCATGTGG, 3' site CACCATGTG), XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTGTCTGCTTCTAAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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lab_host="DH10B"
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strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.8; DB 1;
Pred. No. 6.6e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 785;
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                                                                               EST 18-MAR-1999
clone
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; Murinae; Mus
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ACCESSION
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AGENCOURT 10789306 NIH MGC 152 Mus musculus cDNA clone IMAGE:6766752 5', mRNA sequence.
CA478518
CA478518.1 GI:24936188
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                       91;
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Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
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(bases 1 to 799)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME185-F13; Site 1: DrallI
(CACTGTGTG); Site 2: DrallI (CACATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DrallI adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DrallI sites of the pME185-F13
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to scalud fragater.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used to isolate the cDNA insert. S:
performed to exclude fragments <1.5kb.</pre>
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/clone="IMAGE:1889392"
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/strain="C57BL"
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lab_host="DH10B"
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Pred. No. 6.6e-14;
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                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                 uk28b10.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1970299 5' similar to gb:X81579 M.musculus mRNA for
insulin-like growth factor binding (MOUSE);, mRNA sequence.
                                             Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie, Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schn,Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCa
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 848)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLKM000138 row: m column: 23
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Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 811)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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               Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                            Mus musculus
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Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                   AI790802.1
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/db_xref="taxon:10090"
/clone="IMAGE:6766752"
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Pred. No. 6.6e-14;
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                                                     Cardenas, M., McCann, R.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus 1 (bases 1 to 852)

Marxa, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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/clone lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME185-FL3; Site 1: DraIII
(CACCATGTGT); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
ATGTGGCCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI shoul
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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Pred. No. 6.7e-14;
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                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                            EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ui69d08 yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1887663 5' similar to gb:M59316 rnal INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (HUMAN); gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 605)
                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                            AI196154.1
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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This clone is available royalty-free through LLNL ;
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Fax: 314 286 1810
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                 WashU-HHMI Mouse EST Project
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Location/Qualifiers
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//Clone_lib="Sugano mouse liver mlia"
//Clone_Torgan: liver; Vector: pME38S-FL3; Site_1: DraIII
//CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st Etrand cDNA
was primed with an oligo(dT) primer
[ATCTGGCCTTTTTTTTTTTTTTTTTT], double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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Pred. No. 6.7e-14
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Dubuque, T.

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REFERENCE
AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 380)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                    ui73a06.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1888018 5' similar to gb:X81579 M.musculus mRNA for insulin-like growth factor binding (MOUSE);, mRNA sequence
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                        Mus musculus
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /notes—Torgan: liver; Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCATGTG); lst strand cDNA was primed with an oligo(dT) primer [ATCTGGCCTTTTTTTTTTTTTTTTTTT], double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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/strain="C57BL"
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Pred. No. 1.8e-13;
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Search completed: September Job time: 3217.09 secs

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Best Local Similarity
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                                384 CAGAGAGCTGTGACCACCACCTTCCGCTACTAGCTA 418
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61
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Contact: Warra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                      TCCACTGCCCGCGGAGACACACCCCAGCGAGCATTGAACACTGCATACGGCCGTCTGCC
CAGAGAGCTGTGACCACCATTGCCACTACTATCTA
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                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                               /clone_lib="Sugano mouse liver mlia"
//clone_lib="Sugano mouse liver mlia"
//note="Organ: liver; Vector: pmB:18S-FL3; Site 1: DraIII
/CACCTGTGTGG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
/lab_host="DH10B"
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/clone="IMAGE:1888018"
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/strain="C57BL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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Pred. No. 1.2e-12;
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/2/pubpna/US07_
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Copyright (c) 1993 - 2005
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/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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2248.600 Million cell updates/sec
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US-10-363-483A-40664	-10-363-483A-	-10-363-345A-	-10-363-345A-	-10-719-993-3	-10-719-993-3	0-764-420-94	-10-037-182-	09-845-583-	S-10-719-993-68	-10-719-993-35	-10-741-600-69	-10-085-117-17	-10-756-149-	-10-388-263-38	-10-461-668-1	-10-096-399A	US-10-091-625-11	-10-363-483A-4	-483A-4065	-10-363-345A-4	-363-345A-4065	09-972-916A-6	-10-741-600-179	-10-029-386-518	-10-017-122-1	-10-029-386-	0	-10-152-319A	-10-388-934-	-10-893-315-	-10-893-	S-10-756-149-	US-09-880-107-2393	L	-10-191-803-	US-10-388-934-5	US-09-917-800A-1608
Sequence 40664, A	e 40663,	e 40664,	e 4066	35509	equence 35504,	φ	Sequence 3, Appli	quence 1,	5	35505	•••	172,	Sequence 4571, Ap	381,	11,	Sequence 11, Appl	11,	4066	e 40659,	40660,	40659,	Sequence 6, Appli	equence 1	516	equence	e 203	quence 1, A	equence 2150,	equence 36,	equence 160,	equence 126, F	e 1484,	2393, /	e 16	e 73	Sequence 5, Appli	Sequence 1608, Ap

ALIGNMENTS

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; OTHER INFORMATION: Synthesized
US-09-972-916A-6
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US-09-972-916A-6
                                                                                                                                Query Match
Best Local S
Matches 423
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR APPLICATION NUMBER: US 60/239,113
                                                                                                                                                                                                                                                                                     LENGTH: 423
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                / Match 100.0%; Score 423; DB 9; Length 4:
Local Similarity 100.0%; Pred. No. 2.2e-136;
1es 423; Conservative 0; Mismatches 0; Indels
  61
                                                                               1 CATGGGCGCACGGGGGCACTCCCCGTGGTTCCTGGACTCTGGCCCCCCAGTGTACATGGGCGC
ACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCGCACGGGGCAC 120
                                              CATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCGC
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Sequence 3, Application US/09972916A

Patent No. US20020107198A1

GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 270
TYPE: DNA
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Best Local S
Matches 270
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                                                                   334
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             TGACCACCACTTCCGCTACTAGCTAGCCGC 423
                                           GCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG
                                                           GCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCCAGAGAGCTG
                                                                                                             AAACAAACTTATTTTGAACACGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
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270
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US-09-972-916A-5
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Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 297; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthesized
                                                                     283
                                                                                      334 GCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG 393
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                                 TGACCACCACTTCCGCTACTAGCTAGCCGC 423
                                                                                                                                                           AAACAAACTTATTTTGAACACGGGGGATCCTAGCACGCTGCCCTGACAATCATTAACCCGT
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                                                                     GCCGAGACACAAACCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCCAGAGAGCTG
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Pred. No. 3.9e-67;
0; Mismatches 74;
372
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RESULT 4

US-09-972-916A-4

; Sequence 4, Application US/09972916A
; Patent NO. US20020107198A1
; GENERAL INFORMATION:
; APPLICANT: Thule, Peter M.
; TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR OF INSULIN TRANSCRIPTION
; FILE REFERENCE: US 1292/01 (VA)
; CURRENT APPLICATION NUMBER: US/09/972,916A
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/239,113
; PRIOR APPLICATION NUMBER: US 60/239,113
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 4
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Artificial Sequence

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RESULT 6
US-09-972-916A-5/c.
Sequence 5, Application US/09972916A
Patent No. US20020107198A1
GENERAL INFORMATION:
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE RE
FILE REFERENCE: US 1292/01 (VA)
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US-09-972-916A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
LENGTH: 219
TYPE: DNA
ORGANISM: Rattus norvegicus
PEATURE:
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APPLICANT: Thule, Peter M.
APPLICANT: Thule, Peter M.
TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR
FILE REFERENCE: US 1292/01 (VA)
CURRENT APPLICATION NUMBER: US/09/972,916A
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,113
PRIOR FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 6
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Best Local Similarity
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                                                                                                                                                                                                        CCACTGCCCGCCGAGACACAAACCCCAGCGAGCATTGAACACTGCACACGGCCATCTGCCC
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100.0%; Pred. No. 1.3e-65;
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Pred. No. 1.1e-65;
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                   INSULIN TRANSCRIPTION
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RESULT 8 US-09-917-800A-1608

Sequence 1608, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur

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; FEATURE:
; OTHER INFORMATION:
US-09-972-916A-4
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                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4
LENGTH: 321
TYPE: DNA
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APPLICANT: Thule, Peter M.

APPLICANT: Thule, Peter M.

TITLE OF INVENTION: GLUCOSE SENSITIVE REGULATOR
FILE REFERENCE: US 1992/01 (VA)

CURRENT APPLICATION NUMBER: US/09/972,916A

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/239,113

PRIOR FILING DATE: 2000-10-11

NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                           Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.4%; Score 154; DB 9; Best Local Similarity 100.0%; Pred. No. 5.9e-43; Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                Local Similarity
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  43
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CACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTA 1
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                                                                                ACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGGCG
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                                                                                                                                                         24.3%; Score 103; DB 9; ilarity 100.0%; Pred. No. 2.9e-25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                Length 321
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                                                                                                                                                           Gaps
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FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31

TITLE OF INVENTION: Molecular Toxicology Modeling

Gene Logic,

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; SEQ ID NO 5; LENGTH: 1500; TYPE: DNA; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat) US-10-388-934-5
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-388-934-5
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Publication No. US20040005547A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1608
LENGTH: 1500
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                                                                                                                                                                                                                    FILE REFERENCE: 21199
CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14
                                                                                                                                                              PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 862
                                                                                                                                                                                                                                                                                                                               APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef
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PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
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PRIOR
                                                                                                                                               SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR
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ORGANISM: Rattus norvegicus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-05-15
APPLICATION NUMBER: US 60/292,336
FILING DATE: 2001-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/295,798
FILING DATE: 2001-06-06
APPLICATION NUMBER: US 60/297,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/222,880 FILING DATE: 2000-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/298,884 FILING DATE: 2001-06-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/290,645 FILING DATE: 2001-05-15
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                                                                                                                                               version 3.1
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98.7%;
18.1%;
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Pred. No. 7.9e-16;
Score 76.4; DB 17; Pred. No. 7.9e-16;
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                 Length 1500;
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APPLICANT: Mendrick, Donna
APPLICANT: Donter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT ELING DATE: 2002-05-22
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US-10-152-319A-1613
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-66
NUMBER OF SEQ ID NOS: 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 73
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APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
PRIOR APPLICATION NUMBER: US 60/292,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_013144
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77; Conserv
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Pred. No. 7.9e-16;
0; Mismatches 1;
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APPLICANT: Vockiey, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
FIGURIT: Scherf, Uwe
APPLICANT: Scherf, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION UMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION UMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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                                                                    US-09-880-107-2393
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Best Local S
Matches 77
                                                                                                                                      SOFTWARE: PatentIn Ver.
SEQ ID NO 2393
LENGTH: 6128
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2393, Application Patent No. US20020142981A1
 Query Match .

Best Local Similarity

Matches 141; Conserv
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SEQ ID NO 1613
LENGTH: 1500
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PRIOR APPLICATION NUMBER: US 60/330,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-10-22
                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                    OTHER INFORMATION:
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R APPLICATION N
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/324,928 FILING DATE: 2001-09-27
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APPLICATION NUMBER: US 60/303,810
FILING DATE: 2001-07-10
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APPLICATION NUMBER: US 60/330,462
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                                                                                   Genbank Accession
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98.7%;
                 14.4%;
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 Score 60.8; DB 9; Pred. No. 3.1e-10; 0; Mismatches 52;
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Pred. No. 7.9e-16;
0; Mismatches 1
                                                                                   No.

    See File Wrapper or PALM

                                                                                   US20020142981A1 M74587
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                               Length 6128;
Indels
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; ORGANISM: Homo
US-10-756-149-1484
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US-10-756-149-1484
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                                                                                                                                                                            Sequence 126, Application US/10893315
Publication No. US20050147987A1
GENERAL INFORMATION:
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SEQ ID NO 1484
LENGTH: 6128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 141; Conserv
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000786
CURRENT APPLICATION NUMBER: US/10/893,315
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/231,397
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Aziz, Natasha
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
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CURRENT FILING DATE: 2004-01-12
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Pred. No. 3.1e-10;
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Sequence 160, Application US/10893315

Publication No. US20050147987A1

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL000786

CURRENT APPLICATION UNMEER: US/10/893,315

CURRENT APPLICATION NUMBER: 60/231,397

PRIOR RILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2172

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 160

LENGTH: 9174

TYPE: DNA

ORGANISM: Human

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SOFTWARE: FastSEQ for Windows Version

SEQ ID NO 126

; LENGTH: 9173

TYPE: DNA

; ORGANISM: Human

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US-10-893-315-160
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Search completed: September 1,

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Maximum DB
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length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Match Length DB
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Listing first 45 summaries
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US-08-949-016-12147
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US-09-949-016-1355
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US-09-949-016-1381
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ALIGNMENTS

US-09-949-001-30 RESULT 1

Sequence 30, Application Patent No. 6825336 GENERAL INFORMATION:
APPLICANT: VENTER, J.

Application US/09949001

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR TILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30
LENCTH: 0-7-7

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RESULT 2
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; ORGANISM: Human
US-09-949-001-30
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Best Local Similarity
Matches 141; Conserv
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                                                                     CCATCTGCCCAGAGAGCTGTGACCACCACTTC 406
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                                                       CCACCCTCCCAGAGAGCACTGGCCACCGCTCC 2080
                                                                                                           GAGCATCGGCCACCGCCATCC-----CATCCAGCGAGCATCTGCCGCCGCCGCCGCCG
                                                                                                                                                                TAACCTCCTGGTGCAAGTGGCGCGGCCTGTGCCCCTTTATAAGGTGCGCGCTGTGTCCAGC
                                                                                                                                                                                                                    CACTAGCAMAACAAACTTATTTTGAACACTCAGCTCCTAGCGTGCGGGGGCGCTGCCAATCAT
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Pred. No. 2e-09;
0; Mismatches
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Sequence 36, Application US/09949001
Sequence 36, Application US/09949001
Patent No. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION

OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT FILING DATE: 2003-01-15

FILE REFERENCE: CL000789

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RESULT 3
US-08-945-140-1
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                                          COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/945,140
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/04558
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96/00560
FILING DATE: 14-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SAVILZEY DEG., MARTEIN F.
REGISTRATION NUMBER: 29,699
PRIOR APPLICATION NUMBER: 29,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/231,323
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 9174
TYPE: NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.4%;
Best Local Similarity 66.5%;
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: CHEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                 REFERENCE/DOCKET NUMBER: EX TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GLUCOSE-INDUCIBLE RECOMBINANT VIRAL TITLE OF INVENTION: VECTOR NUMBER OF SEQUENCES: 10
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APPLICANT: KAHN, Axel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA
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500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
(610)
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Pred. No. 2e-09;
0; Mismatches 52;
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Matches
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GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                  ORIGINAL SOURCE:
ORGANISM: rat
FEATURE:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 13011 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Makoto MURASE et al.
TITLE OF INVENTION: Method for Increasing Stora
TITLE OF INVENTION: Lipid Content in Plant Seed
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/791,849A FILING DATE: January 30, 1997 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                     NTI-SENSE:
                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                     TOPOLOGY:
                                                                                                                                                 STRANDEDNESS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                       TELEPHONE:
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o. 5914449
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Makoto MURASE et al.
VENTION: Method for Increasing Storage
                                                                                                                                 linear
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join(3212..3218, 3766..3948, 5917..6008, 6152..6283, 6418..6604, 6921..7191, 7302..7452, 7665..7817, 7911..8077
                                 SGD
                                                                  rat (Rattus norvegicus)
                                                                                                                                                                                                                                                                        202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette, 3.5 inch, 1.44
                                                                                                                   DNA (genomic)
                                                                                                                                                   double
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Pred. No. 2.4e-08;
0; Mismatches 8;
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US-09-949-016-16965/c
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RESULT 6
US-09-949-016-12147
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US-09-949-016-16965
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Best Local S
Matches 60
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 16965
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                  Matches 103; Conservative
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 40586
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                                                                                                                                                      AGGCGAGGTGTCCCCACAGT
                                                                                          TEGACTCTEGCCCCCAGTGT
                                                                                                                        Conservative
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6284..6417, 6605..6920, 7191..7301, 7453..7664, 7818..7910,
9480..10162)
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6152..6283, 6418..6604, 6921..7191, 7302..7452,
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Pred. No. 0.00073;
0; Mismatches 97; Indels 0;
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Pred. No. 1.6e-07;
0; Mismatches 8;
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OF DETECTION AND USES THEREOF
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12147
LENGTH: 767677
                                                                 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 17361 LENGTH: 767677
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17361, Appl. Patent No. 6812339
GENERAL INFORMATION:
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                  PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
FEATURE:
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LOCATION: (1)...(767677)
OTHER INFORMATION: n = A,T,C or G
ORGANISM: Human FEATURE:
                                                TYPE: DNA
                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       562508 GCCCC 562512
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Local Similarity 51.4%;
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OF DETECTION AND USES THEREOF
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NAME/KEY: misc_feature

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
VUMBER FILING DATE: 2000-09-08
VUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASSEQ for Windows Version 4.0
SEQ ID NO 11786
LENGTH: 15108
                                                                                                                                                                US-09-949-016-17205
                                                                                                                                                                                     RESULT 9
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; OTHER INFORMATION: n = A
US-09-949-016-17361
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Sequence 17205, Application US/09949016
Patent NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIOF ILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: CL001307
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ORGANISM: Human
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OF DETECTION AND USES
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTMARE: FastSEQ for Windows Version 4.
SEQ ID NO 17205
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Matches
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Matches
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CURRENT APPLICATION NUMBER: US/09/845,583A
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/200,863
PRIOR FILING DATE: 2000-05-01
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APPLICANT: Brunken, William Joseph
APPLICANT: Champliaud, Marie-France
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SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
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ORGANISM: Mus musculus
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6044 CCTGTGGTCCCTGGCTGGCAGTGACACTGACCGCTCTGAG 6005
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Pred. No. 0.015;
0; Mismatches
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RESULT 11 US-09-949-016-12957 ; Sequence 12957, Application US/09949016 ; Patent No. 6812339

GENERAL INFORMATION:

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-12208
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 12208
LENGTH: 30244
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SEQ ID NO 12957
LENGTH: 35471
                                                                                 Matches
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NAME/KEY: misc_feature
LOCATION: (1)...(35471)
OTHER INFORMATION: n = A,T,C or
3-09-949-016-12957
                                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
13568 GCCAGCTGTACATCTGGGTGCTCTGGGGACCCGGGCGTTCACGGCATGTTGCCCTGGGT 13627
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                                       GCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGT 99
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                                                                                 Conservative
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                                                                                                  8.7%;
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                                                                              Score 36.8; DB Pred. No. 0.28; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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OF DETECTION AND USES
                                                                                                                    Length 30244;
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SOFTWARE: PER SEQ ID NO 138 LENGTH: 3054

PERL Program

TYPE: DNA ORGANISM: Homo

sapiens

FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 336987.1CB1

GENERAL INFORMATION:

APPLICANT: Jones, Karen A. APPLICANT: Volkmuth, Wayne APPLICANT: Walker, Michael

APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172

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US-09-484-970B-138
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US-09-949-016-13550
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US-09-949-016-13550
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Sequence 138, Application US/09484970B Patent No. 6426186
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Best Local :
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LENGTH: 30245
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
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les 92; Conserv
                                                                                                                                13686
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                                                                                                                                TGCTCTGGGGACCCGGGTGGTTCATGGCATGTTGCCCCTGGGTTTTT 13731
                                                                                                                                                                                                                                                          GTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTACATGGG 159
                                                                                                                                                                        CGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAGTGTAT 205
                                                                                                                                                                                                                                                                                                         GCCAGCTGTACATCTGGGTGCTCTGGGGACCCGGGCGGTTCACGGCATGTTGCCCTGGGT 13627
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55.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13841
LENGTH: 134008
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                   ; FRATURE:

NAME/KBY: misc_feature

; LOCATION: (1)...(134008)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13841
Search completed: September Job time: 139.759 secs
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US-09-949-016-13841
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 85
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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Best Local Similarity
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                                                                             CTGGACGCACGACGACGTGGACGCACGGATGACTCAGATCCCCAG 127237
                                                                                                               ATGGGCGCACGGGCACTCCCGTGGTTCCTGGACTCTGGCCCCCAG 200
                                                                                                                                                                                                                                   CACGGACACCCAGACGACGCGCACAGACGACGCGCGCACACACACAGATGACGTGGACGC 127131
                                                                                                                                                                                                                                                                        CTCTGGCCCCAGTGTACATGGGCGCACGGGGCACTCCCGTGGTTCCTGGACTCTGGCCC 94
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